

FIG. 1

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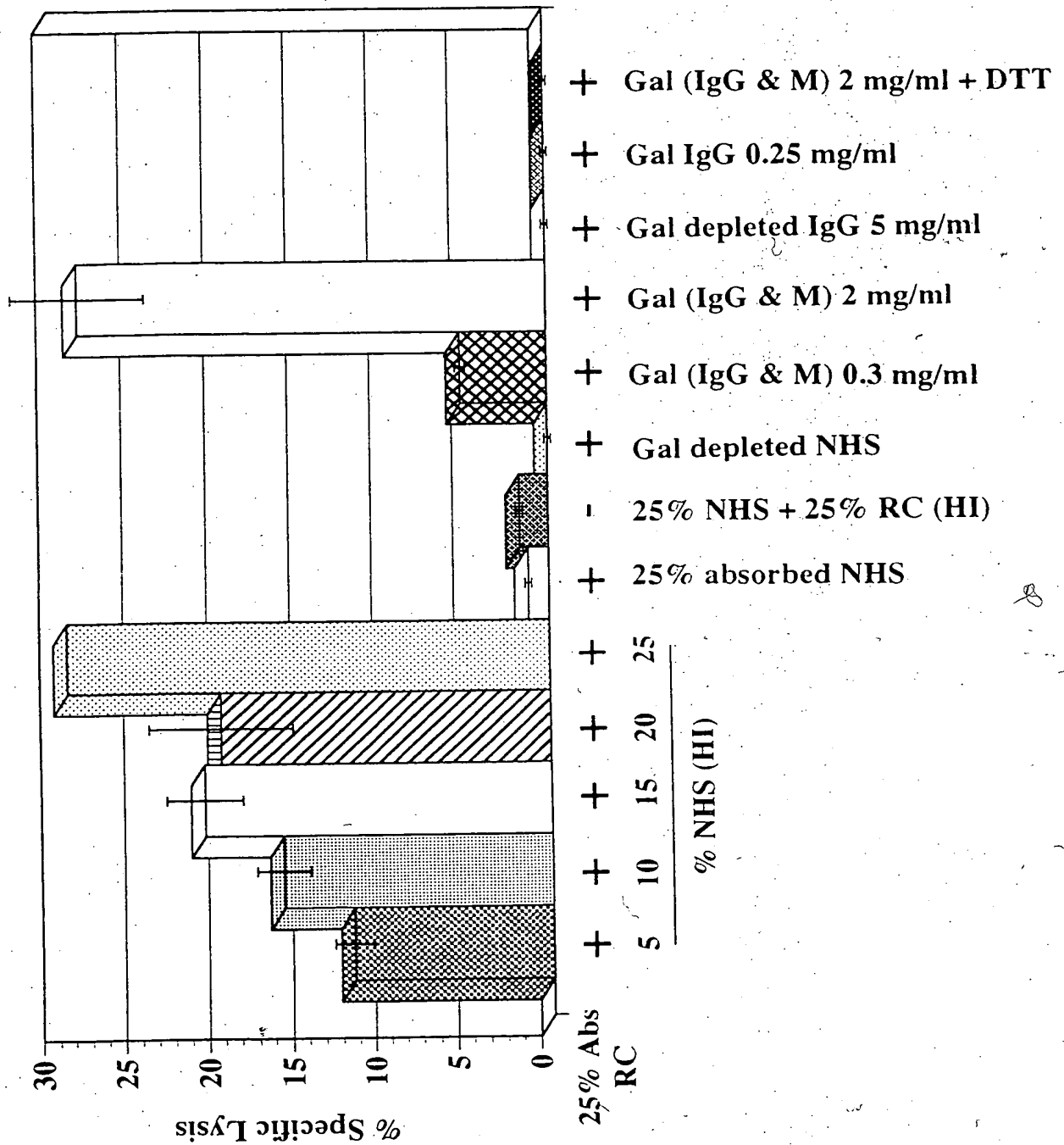


FIG. 2

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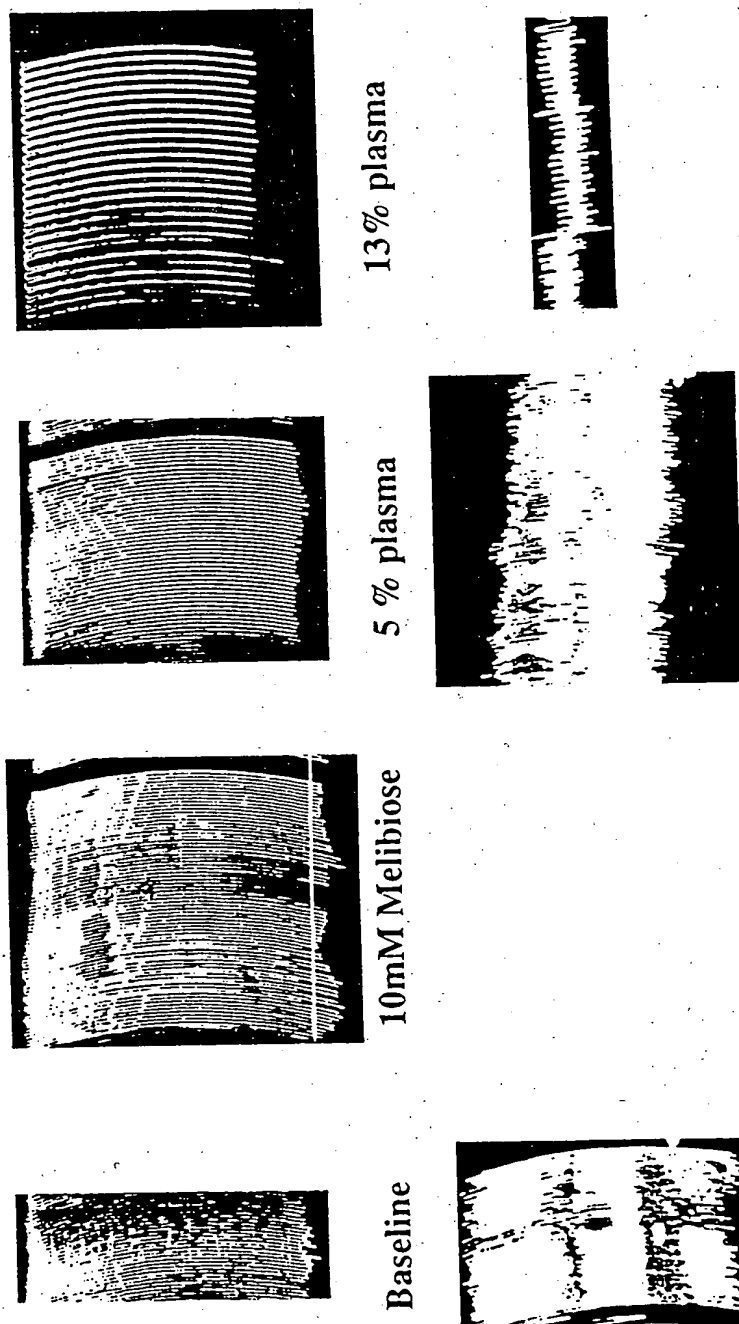


FIG. 3

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PGTCD	1	-----	-----	-----	-----	-----	-----	50
BOVGSTA	1	CCGGGGGCGG	GGCCGAGCTG	GGAGCGTCGA	GCCCGCTGCC	CAGCGCCCGC	-----	50
MUSGLYTNS	1	-----	-----	-----	-----	-----	-----	50
PGTCD	51	-----	-----	-----	-----	-----	-----	100
BOVGSTA	51	CGGCTCCCTC	GCGCCCTTGC	CCGCCGCCCC	GGAGGAGCGC	CCGGCGGCGG	-----	100
MUSGLYTNS	51	-----	-----	-----	-----	-----	-----	100
PGTCD	101	-----	-----	-----	-----	-----	-----	150
BOVGSTA	101	GCCGACGGGA	GCGCAGCGGC	ACACCCCGCC	CCGGCACGCC	CGCGGGGCTC	-----	150
MUSGLYTNS	101	-----	-----	-----	-----	-----	-----	150
PGTCD	151	-----	-----	-----	-----	-----	-----	200
BOVGSTA	151	GGGAGGAGGC	AGCGCGCCGA	CTGTTCCGGC	AGCCGAGGAC	GCCGCCGGGG	-----	200
MUSGLYTNS	151	-----	-----	-----	-----	-----	-----	200
PGTCD	201	-----	-----	-----	-----	-----	-----	250
BOVGSTA	201	AGCCGAGGCG	CCGGCCAGCC	CCCAGCGCGC	CCAGCTTCTG	CGGATCAGGG	-----	250
MUSGLYTNS	201	-----CG	TCITTAGGAG	CTGGAGATTC	TGGGTGGAGC	CCTAGCCCCG	-----	250
PGTCD	251	-----	-----	-----	-----	-----	-----	300
BOVGSTA	251	AAACCACGTG	TCCTCAAGTG	GCCAGCCAGC	TGTCCCCAAG	AGGAACCTGC	-----	300
MUSGLYTNS	251	CCTTTTCTTA	GCTGGCTGAC	ACCTTCCCTT	GTAGACTCTT	CTTGGAATGA	-----	300
PGTCD	301	-----	-----	-----	-----	-----	-----	350
BOVGSTA	301	CTGGCATTTG	CACGGAAAGA	CGAGACACTT	CACAAAATCA	ACGGAGTCAG	-----	350
MUSGLYTNS	301	GAAGTACCGA	TTCTGCTGAA	GACCTCGCGC	TCTCAGGCTC	TGGGAGTTGG	-----	350

Exon 1 Exon 2

FIG. 4A

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PGTCD	351	-----	-----	-----AGC	CCTGCCCTCCT	TCTGCAGAGC	400
BOVGSTA	351	AAGGCTGCAC	CTTCGCTTCC	TCCC-----AGC	CCTGCCCTCCT	TCTGCAGAAC	400
MUSGLYTNS	351	AACCCCTGTAC	CTTCCTTTTCC	TCTGCTGAGC	CCTGCCCTCCT	TGGGCAGGCC	400
PGTCD	401	AGAGCTCACT	AGAACTT-GT	TTC-----GCC	TTTTACTCTG	GGGGGAGAGA	450
BOVGSTA	401	GGAGCTCAGT	AGAACTT-GG	TACTTTTGCC	TTTTACTCTA	GGAGGAGAGA	450
MUSGLYTNS	401	AGAGCTCGAC	AGAACTCTCGG	TTGCTTTGCT	GTTTGCTTTG	GAGGGAACAC	450
			Exon 2 Exon 3				
PGTCD	451	AGCAGAGGAT	GAG-----	-----	-----	-----	500
BOVGSTA	451	AGCAGACGAT	GAG-----	-----	-----	-----	500
MUSGLYTNS	451	AGCTGACGAT	GAGGCTGACT	TTGAACTCAA	GAGATCTGCT	TACCCCGATC	500
PGTCD	501	-----	-----	-----	-----	-----	550
BOVGSTA	501	-----	-----	-----	-----	-----	550
MUSGLYTNS	501	TCCTGGAATT	AAAGGCCTGT	ACTACCTTGC	CTGGACCTAA	GATTTTCATG	550
PGTCD	551	-----	-----	-----	-----	-----	600
BOVGSTA	551	-----	-----	-----	-----	-----	600
MUSGLYTNS	551	ATCACTATGC	TTCAAGATCT	CCATGTCAAC	AAGATCTCCA	TGTCAAGATC	600
			Exon 3 Exon 4				
PGTCD	601	-----	-----	-----	-----	---GAGAAAA	650
BOVGSTA	601	-----	-----	-----	-----	---GAGAAAA	650
MUSGLYTNS	601	CAAGTCAGAA	ACAAGTCTTC	CATCCTCAAG	ATCTGGATCA	CAGGAGAAAA	650
PGTCD	651	TAATGAATGT	CAAAAGGAAGA	GTGGTTCTGT	CAATGCTGCT	TGCTCTCAACT	700
BOVGSTA	651	TAATGAATGT	CAAAAGGAAAA	GTGATTCTGT	CAATGCTGGT	TGCTCTCAACT	700
MUSGLYTNS	651	TAATGAATGT	CAAGGGAAAA	GTAATCCTGT	TGATGCTGAT	TGCTCTCAACC	700
			Start				

FIG. 4B



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MATERIALS AND METHODS FOR MANAGEMENT OF HYPERACUTE REJECTION IN HUMAN
XENOTRANSPLANTATION

Anthony J.F. D'Apice et al.

08/984,900

07039-473002

PGTCD	701	GTAATGGTTG	TGTTTTGGGA	ATACATCAAC	AGCCCAGAAG	GTTCTTTGTT	750	Exon 4	Exon 5
BOVGSTA	701	GTCATTGTTG	TGTTTTGGGA	ATATATCCAC	AGCCCAGAAG	GCTCTTTGTT	750		
MUSGLYTNS	701	GTGGTTGTCG	TGTTTTGGGA	ATATGTCAAC	AGCCCAGACG	GCTCTTTCTT	750		
PGTCD	751	CTGGATATAC	CAGTCAAAAA	ACCCAGAAAGT	TGGCAGCAGT	GCTCAGAGGG	800	Exon 5	Exon 6
BOVGSTA	751	CTGGATAAAC	CCATCAAGAA	ACCCAGAAAGT	TGGTGGCAGC	AGCATTCAGA	800		
MUSGLYTNS	751	GTGGATATAT	CACACAAAAA	TTCCAGAGGT	TGGTGAGAAC	AGATGGCAGA	800	Exon 6	Exon 7
PGTCD	801	GCTGGTGG--	-TTTCCGAGC	TGGTTTAAAC	ATGGGACTCA	CAGTTACCAC	850		
BOVGSTA	801	AGGCTGGTG	GCTTCCGAGA	TGGTTTAAAC	ATG-----	--GTTACCAT	850		
MUSGLYTNS	801	AGGACTGGTG	GTTCCCAAGC	TGGTTTAAAA	ATGGGACCCA	CAGTTATCAA	850		
PGTCD	851	GAAGAAGAAG	ACGCTATAGG	CAACGAAAAG	GAACAAAGAA	AAGAAGACAA	900		
BOVGSTA	851	GAAGAAGATG	GAGACATAAA	CGAAGAAAAG	GAACAAAGAA	ACGAAGACGA	900		
MUSGLYTNS	851	GAAGACAACG	TAGAAGGACG	GAGAGAAAAG	GGTAGAAAATG	GAGATCGCAT	900	Exon 7	Exon 8
PGTCD	901	CAGAGGAGAG	CTTCCGCTAG	TGGACTGGTT	TAATCCTGAG	AAACGCCCCAG	950		
BOVGSTA	901	---AAGCAAG	CTTAAGCTAT	CGGACTGGTT	CAACCCATTT	AAACGCCCCCG	950		
MUSGLYTNS	901	---TGAAGAG	CCTCAGCTAT	GGGACTGGTT	CAATCCAAAG	AACC GCCCCG	950		
PGTCD	951	AGGTCGTGAC	CATAACCAGA	TGAAGGCTC	CAGTGGTATG	GGAAGGCACT	1000		
BOVGSTA	951	AGGTTGTGAC	CATGACGAAG	TGAAGGCTC	CAGTGGTGTG	GGAAGGCACT	1000		
MUSGLYTNS	951	ATGTTTGTGAC	AGTGACCCCG	TGAAGGCGC	CGATTGTGTG	GGAAGGCACT	1000		
PGTCD	1001	TACAACAGAG	CCGTCTTTAGA	TAATTATTAT	GCCAAACAGA	AAATTACCGT	1050		
BOVGSTA	1001	TACAACAGAG	CCGTCTTTAGA	CAATTATTAT	GCCAAGCAGA	AAATTACCGT	1050		
MUSGLYTNS	1001	TATGACACAG	CTCTGCTGGA	AAAGTACTAC	GCCACACAGA	AACTCACTGT	1050		

FIG. 4C



		Exon 8 Exon 9	
PGTCD	1051	GGGCTTGACG GTTTTGTCTG TCGGAAGATA CATTGAGCAT TACTTGGAGG	1100
BOVGSTA	1051	CGGCCTGACG GTTTTCGCCG TCGGAAGATA CATTGAGCAT TACTTGGAGG	1100
MUSGLYTNS	1051	GGGGCTGACA GTGTTTGTCTG TCGGAAAGTA CATTGAGCAT TACTTAGAAG	1100
PGTCD	1101	AGTTCTTTAAT ATCTGCAAAAT ACATACITTC TGGTTGGCCA CAAAGTCATC	1150
BOVGSTA	1101	AGTTCTTTAAC GTCTGCTAAT AAGCACTTCA TGGTGGGCCA CCCAGTCATC	1150
MUSGLYTNS	1101	ACTTTCCTGGA GTCTGCTGAC ATGTACITTC TGGTTGGCCA TCGGGTCATA	1150
PGTCD	1151	TTTTTACATCA TGGTGGATGA TATCTCCAGG ATGCCCTTTGA TAGAGCTGGG	1200
BOVGSTA	1151	TTTTTATATCA TGGTAGATGA TGTCTCCAGG ATGCCCTTTGA TAGAGTTGGG	1200
MUSGLYTNS	1151	TTTTTACGTCA TGATAGATGA CACCTCCCGG ATGCCCTGTCG TGCACCTGAA	1200
PGTCD	1201	TCCTCTGCGT TCCTTTAAAG TGTTTGAGAT CAAGTCCGAG AAGAGGTGGC	1250
BOVGSTA	1201	TCCTCTGCGC TCCTTCAAAG TGTTTAAGAT CAAGCCTGAG AAGAGGTGGC	1250
MUSGLYTNS	1201	CCCTCTACAT TCCTTACAAG TCTTTGAGAT CAGGTCTGAG AAGAGGTGGC	1250
PGTCD	1251	AAGACATCAG CATGATGCGC ATGAAGACCA TCGGGGAGCA CATCCTGGCC	1300
BOVGSTA	1251	AGGACATCAG CATGATGCGC ATGAAGACTA TCGGGGAGCA CATTGTGGCC	1300
MUSGLYTNS	1251	AGGATATCAG CATGATGCGC ATGAAGACCA TTGGGGAGCA CATCCTGGCC	1300
PGTCD	1301	CACATCCAGC ACGAGGTGGA CTTCTCTTTC TGCATGGACG TGGATCAGGT	1350
BOVGSTA	1301	CACATCCAGC ATGAGGTTGA CTTCTTTTTC TGCATGGATG TGGACCCAGT	1350
MUSGLYTNS	1301	CACATCCAGC ACGAGGTGGA CTTCTCTTTC TGCATGGACG TGGATCAAGT	1350
PGTCD	1351	CTTCCAAAAC AACTTTGGGG TGGAGACCCCT GGGCCAGTCG GTGGCTCAGC	1400
BOVGSTA	1351	CTTCCAAGAC AAGTTTGGGG TGGAGACCCCT GGGCCAGTCG GTGGCCCCAGC	1400
MUSGLYTNS	1351	CTTTC AAGAC AACTTCGGGG TGGAAACTCT GGGCCAGCTG GTAGCACAGC	1400

FIG. 4D

PGTCD	1401	TACAGGCCTG	GTGGTACAAG	GCACATCCTG	ACGAGTTCAC	CTACGAGAGG	1450
BOVGSTA	1401	TACAAGCCTG	GTGGTACAAG	GCAGATCCCA	ATGACTTCAC	CTACGAGAGG	1450
MUSGLYTNS	1401	TCCAGGCCTG	GTGGTACAAG	GCCAGTCCCG	AGAAAGTTCAC	CTATGAGAGG	1450
PGTCD	1451	CGGAAGGAGT	CCGCAGCCTA	CATTCCGTTT	GGCCAGGGGG	ATTTTATTAA	1500
BOVGSTA	1451	CGGAAGGAGT	CTGCAGCATA	CATTCCCTTC	GGCGAAGGGG	ATTTTATTAA	1500
MUSGLYTNS	1451	CGGGAAGTGT	CGGCCGCGTA	CATTCCATTC	GGAGAGGGGG	ATTTTACTAA	1500
PGTCD	1501	CCACGCAGCC	ATTTTGGGG	GAAACCCAC	TCAGGTTCTA	AACATCACTC	1550
BOVGSTA	1501	CCATGCAGCC	ATTTTGGGG	GAAACCCAC	TCAGGTCCTT	AACATCACCC	1550
MUSGLYTNS	1501	CCACGCGGCC	ATTTTGGAG	GAACGCTAC	TCACATTCTC	AACCTCACCA	1550
PGTCD	1551	AGGAGTGCTT	CAAGGGAATC	CTCCAGGACA	AGGAAAATGA	CATAGAAGCC	1600
BOVGSTA	1551	AGGAATGCTT	CAAGGGAATC	CTCAAGGACA	AGAAAATGA	CATAGAAGCC	1600
MUSGLYTNS	1551	GGGAGTGCTT	TAAGGGGATC	CTCCAGGACA	AGAAAACATGA	CATAGAAGCC	1600
PGTCD	1601	GAGTGGCATG	ATGAAAGCCA	TCTAAACAAG	TATTTCCCTC	TCAACAAAACC	1650
BOVGSTA	1601	CAATGGCATG	ATGAAAGCCA	TCTAAACAAG	TATTTCCCTC	TCAACAAAACC	1650
MUSGLYTNS	1601	CAGTGGCATG	ATGAGAGCCA	CCTCAACAAA	TACTTCCCTT	TCAACAAAACC	1650
PGTCD	1651	CACTAAAATC	TTATCCCCAG	AATACTGCTG	GGATTATCAT	ATAGGCATGT	1700
BOVGSTA	1651	TACTAAAATC	TTATCCCCCG	AATACTGCTG	GGATTATCAC	ATAGGCCTAC	1700
MUSGLYTNS	1651	CACTAAAATC	CTATCTCCAG	AGTATTGCTG	GGACTATCAG	ATAGGCCTGC	1700
PGTCD	1701	CTGTGGATAT	TAGGATTGTC	AAGATAGCTT	GGCAGAAAAA	AGAGTATAAT	1750
BOVGSTA	1701	CTGCGGATAT	TAAAGCTTGC	AAGATGCTT	GGCAGACAAA	AGAGTATAAT	1750
MUSGLYTNS	1701	CTTCAGATAT	TAAAAGTGC	AAGGTAGCTT	GGCAGACAAA	AGAGTATAAT	1750

FIG. 4E

PGTCD	1751	TTGGTTAGAA	ATAACATCTG	ACTTTAAATT	GTGCCAGCAG	TTTTCTGAAT	1800
BOVGSTA	1751	GTGGTTAGAA	ATAATGTCTG	ACTT-----T	GTGCCAGTAC	ATTTCTGAAT	1800
MUSGLYTNS	1751	TTGGTTAGAA	ATAATGTCTG	ACTTCAAATT	GTG-----	--ATGGAAC	1800
				Stop			
PGTCD	1801	TTGAAAGAGT	ATTACTCTGG	CTACTTCCTC	AGAGAAGTAG	---CACTTAA	1850
BOVGSTA	1801	TTGAGAGAGT	ATTATTCTGG	CTACTTCCTC	AGAAAAGTAA	---CACTTAA	1850
MUSGLYTNS	1801	TTGACAC--T	ATTACTCTGG	CTAATTCCTC	AAACAAGTAG	CAACACTTGA	1850
PGTCD	1851	TTTTAACTTT	TAAAAAATA	CTAACAAA-	----TACCAA	CACAGTAA-G	1900
BOVGSTA	1851	TTTTAACTTA	AAAAAATA	CTAACAAA-	----GACCAA	CACAGCAA-A	1900
MUSGLYTNS	1851	TTTCAACTTT	TAAAGAA-A	CAATCAAAAC	CAAAACCCAC	TACCATGGCA	1900
PGTCD	1901	TACATATTAT	TCCTCCTG	AACCTTGAGC	CTTGTCAAAT	GGGAGAAATGA	1950
BOVGSTA	1901	TACATATTAT	TTCTCCTTGT	AACCTTGAGC	CTTGTAATAC	GGGAGAAATGA	1950
MUSGLYTNS	1901	AACAGATGAT	TTCTCCT-GA	CACCTTGAGC	CT-GTAATAT	GTGAGAAAGA	1950
PGTCD	1951	CTCTGTGG--	--TAATCAGA	TGTAAATTCC	CAGTGATTTC	2000
BOVGSTA	1951	ACCTGTGG--	--TAATCAGA	TGTAAATTCC	CAGTGATTTC	TTACCTATT	2000
MUSGLYTNS	1951	GTCTATGGCA	AGTAATCAGG	TATAAATTCT	CAATGATTTC	TTATATATTC	2000
PGTCD	2001	2050
BOVGSTA	2001	TTGGTTGTGG	GGCGGGGAA	TGGATACACC	ATCAGTTGAA	CC.....	2050
MUSGLYTNS	2001	TGGGTCTTGG	GAAACTTGA	TTCTAGAAAT	CAAAATTAAT	TTGACAAAGG	2050
PGTCD	2051	2100
BOVGSTA	2051	2100
MUSGLYTNS	2051	AAAAGCAGAT	GCCGGAAACT	TCTTCCAGT	CTGTACATACA	ATTCACCACT	2100

FIG. 4F

PGTCD	2101
BOVGSTA	2101
MUSGLYTN	2101	GCCAGGTGC	TGAGAAGC	ATTAGGAAC	AGTGCGGT	GTGTCAGAGT	GTGTCAGAGT	GTGTCAGAGT	GTGTCAGAGT	GTGTCAGAGT	GTGTCAGAGT
PGTCD	2151
BOVGSTA	2151
MUSGLYTN	2151	TGGACGGCTC	CATCCCCTTG	GCTTCATTAT	CTTCTCCTC	ATGGAGATTC	ATGGAGATTC	ATGGAGATTC	ATGGAGATTC	ATGGAGATTC	ATGGAGATTC
PGTCD	2201
BOVGSTA	2201
MUSGLYTN	2201	TAAAGCAACC	CAGAGAGGCT	TTGCAGCCAG	AGACCTTTAA	TAAGGATGCC	TAAGGATGCC	TAAGGATGCC	TAAGGATGCC	TAAGGATGCC	TAAGGATGCC
PGTCD	2251
BOVGSTA	2251
MUSGLYTN	2251	AATGTGACCA	TCAGTCTGTA	AAAGCTGATG	GCTCCAGGAG	CGCTGGCAGT	CGCTGGCAGT	CGCTGGCAGT	CGCTGGCAGT	CGCTGGCAGT	CGCTGGCAGT
PGTCD	2301
BOVGSTA	2301
MUSGLYTN	2301	CCAGGCCCCA	CTAGGCTATT	GTTTCTGTCC	TGGGCATAAA	GGAGGCAGAG	GGAGGCAGAG	GGAGGCAGAG	GGAGGCAGAG	GGAGGCAGAG	GGAGGCAGAG
PGTCD	2351
BOVGSTA	2351
MUSGLYTN	2351	AGTGCCAATA	GGTACTTTGG	TGGCACATGT	TCAGAGTCCA	GGAAAAATCA	GGAAAAATCA	GGAAAAATCA	GGAAAAATCA	GGAAAAATCA	GGAAAAATCA
PGTCD	2401
BOVGSTA	2401
MUSGLYTN	2401	AGGCTGACCA	CTTAGAGCGA	CATAGGACTT	GGGTTGGTG	ATTGAACTGA	ATTGAACTGA	ATTGAACTGA	ATTGAACTGA	ATTGAACTGA	ATTGAACTGA

FIG. 4G

FIG. 4H

FIG. 4H

[illegible]

FIG. 41



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	Ex4 ▼	Ex5	Ex5 ▼	Ex6	
PGT[Frame 1]	1	MNVKGRVVL	MLLVSTVMV	FWEYINSPEG	SLFWIYQSKN PEVG-SSAQR 50
BGT[Frame 1]	1	MNVKGVIL	MLVSTVIV	FWEYIHSPEG	SLFWINPSRN PEVGSSIQR 50
MGT[Frame 1]	1	MNVKGVILL	MLIVSTVVV	FWEYVNSPDG	SFLWIYHTKI PEVGENRWQK 50

	Ex6 ▼	Ex7	Ex7 ▼	Ex8	
PGT[Frame 1]	51	GWFPSPWNN	GTHSYHEED	AIGNEKEQRK	EDNRGELPLV DWFNPEKRPE 100
BGT[Frame 1]	51	GWLPSPWNN	G---YHEEDG	DINEEKEQRN	ED-ESKLKLS DWFNPFKRPE 100
MGT[Frame 1]	51	DWWFPSPWFKN	GTHSYQEDNV	EGRREK-GRN	GDRIEEPQLW DWFNPKNRPD 100

	Ex8 ▼	Ex9	
PGT[Frame 1]	101	VVTITRWKAP	VWEGTYNRA VLDNYNKAKQK ITVGLTVFAV GRYIEHYLEE 150
BGT[Frame 1]	101	VVTMTKWKAP	VWEGTYNRA VLDNYYAKQK ITVGLTVFAV GRYIEHYLEE 150
MGT[Frame 1]	101	VLTVTPWKAP	IVWEGTYDTA LLEKYYATQK LTVGLTVFAV GRYIEHYLED 150

PGT[Frame 1]	151	FLISANTYFM	VGHKVIFYIM VDDISRMPLI	ELGPLRSFKV FEIKSEKRWQ 200
BGT[Frame 1]	151	FLTSANKHFM	VGHPVIFYIM VDDVSRMPLI	ELGPLRSFKV FKIKPEKRWQ 200
MGT[Frame 1]	151	FLESADMYFM	VGHRVIFYIM IDDTSRMPV	HLNPLHSLQV FEIRSEKRWQ 200

FIG. 5A

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PGT[Frame 1]201 DISMMRMKTI GEHILAHIQH EVDFLFCMDV DQVFQNNFGV ETLGQSVACL 250
BGT[Frame 1]201 DISMMRMKTI GEHIVAHIQH EVDFLFCMDV DQVFQDKFGV ETLGESVACL 250
MGT[Frame 1]201 DISMMRMKTI GEHILAHIQH EVDFLFCMDV DQVFQDNFGV ETLGQLVACL 250

PGT[Frame 1]251 QAWYKAHPD EFTYERRKES AAYIPFGQGD FYYHAAIFGG TPTQVLNITQ 300
BGT[Frame 1]251 QAWYKADPN DFTYERRKES AAYIPFGEGD FYYHAAIFGG TPTQVLNITQ 300
MGT[Frame 1]251 QAWYKASPE KFTYERRELS AAYIPFGEGD FYYHAAIFGG TPTHILNLTR 300

PGT[Frame 1]301 ECFKGILQDK ENDIEAEWHD ESHLNKYFLL NKPTKILSPE YCWDYHIGMS 350
BGT[Frame 1]301 ECFKGILKDK KNDIEAQWHD ESHLNKYFLL NKPTKILSPE YCWDYHIGLP 350
MGT[Frame 1]301 ECFKGILQDK KHDIEAQWHD ESHLNKYFLF NKPTKILSPE YCWDYQIGLP 350

PGT[Frame 1]351 VDIKIVKIAW QKKEYNLVRN NI*..... 400
BGT[Frame 1]351 ADIKLVKMSW QTKEYNVVRN NV*..... 400
MGT[Frame 1]351 SDIKSVKVAW QTKEYNLVRN NV*..... 400
```

FIG. 5B



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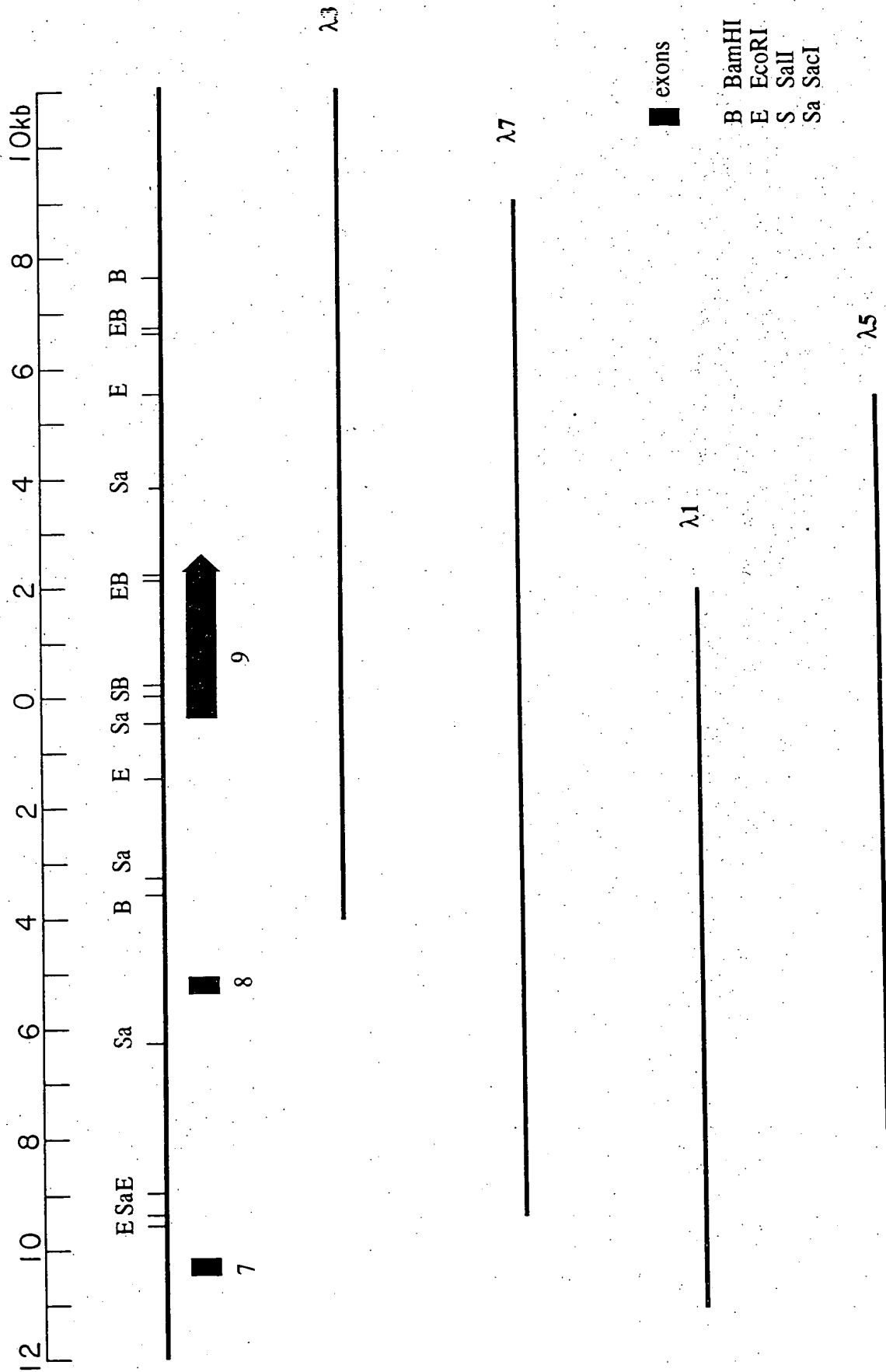
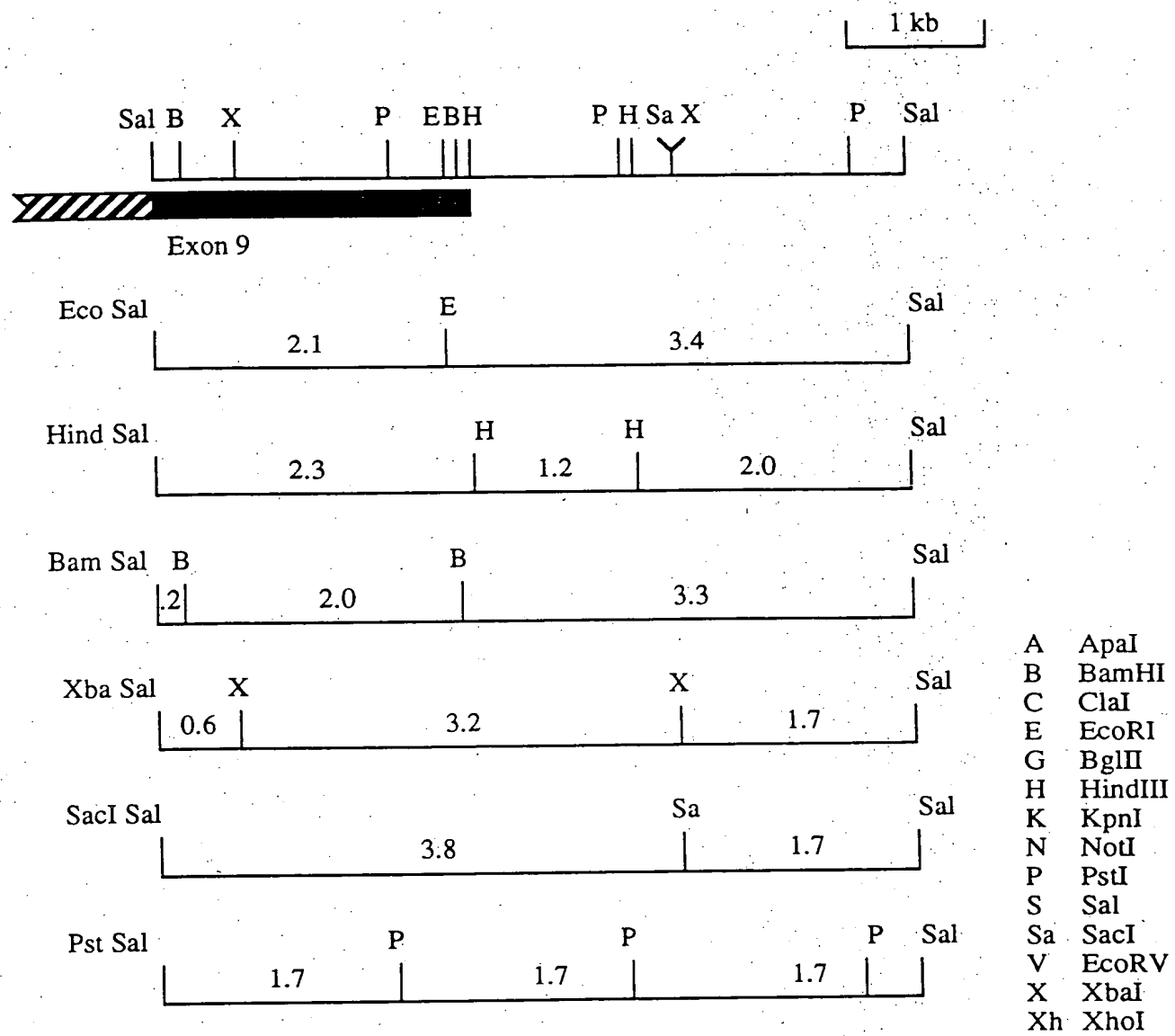


FIG. 6

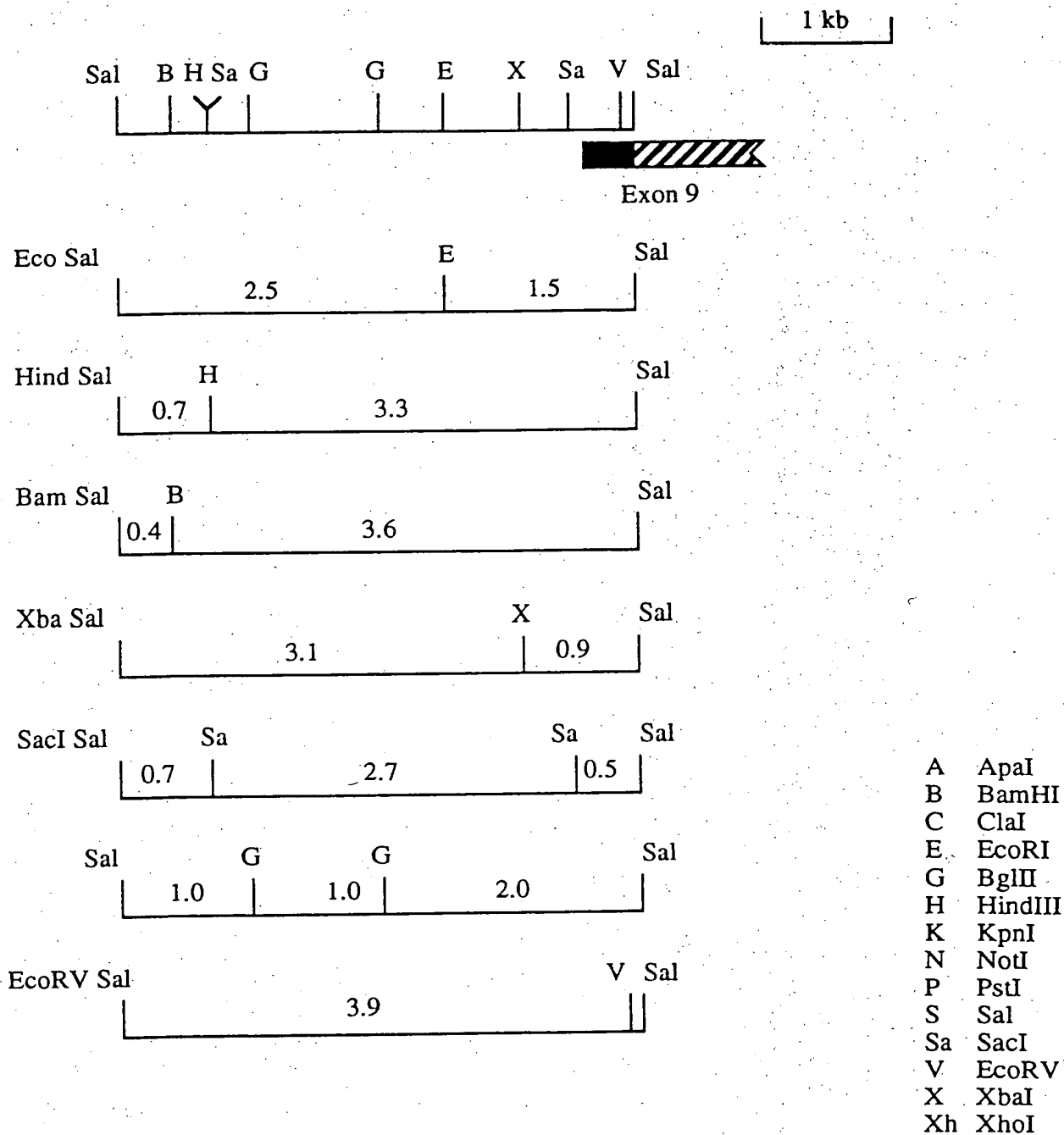


No sites for: BglII, Nde, PvuI, Xho, Kpn, SacII, EcoRV, Sma, Cla, Apa, Not

pBS+KS: SacI SacII Not Xba Spe Bam Sma Pst Eco RV Hind Cla Sal Xho Apa Kpn



FIG. 7



No sites for: Nde, PvuI, Xho, Kpn, SacII, Sma, Cla, Apa, Not

Unmapped sites for: Pst, PvuII

pUBS:

.... SacI SacII Not Xba Spe Bam Sma Pst Eco RV Hind Cla Sal Xho Apa Kpn

FIG. 8



A Apal
B BamHI
C ClaI
E EcoRI
G BglII
H HindIII
K KpnI
N NotI
P PstI
S SalI
Sa SacI
V EcoRV
X XbaI
Xh XhoI

No sites for: Xho, Kpn, SacII, Sma, Cla, EcoRV, Apa, Not, PvuI, Nde

pUBS:

.... SacI SacII Not Xba Spe Bam Sma Pst Eco RV Hind Cla Sal Xho Apa Kpn



FIG. 9b

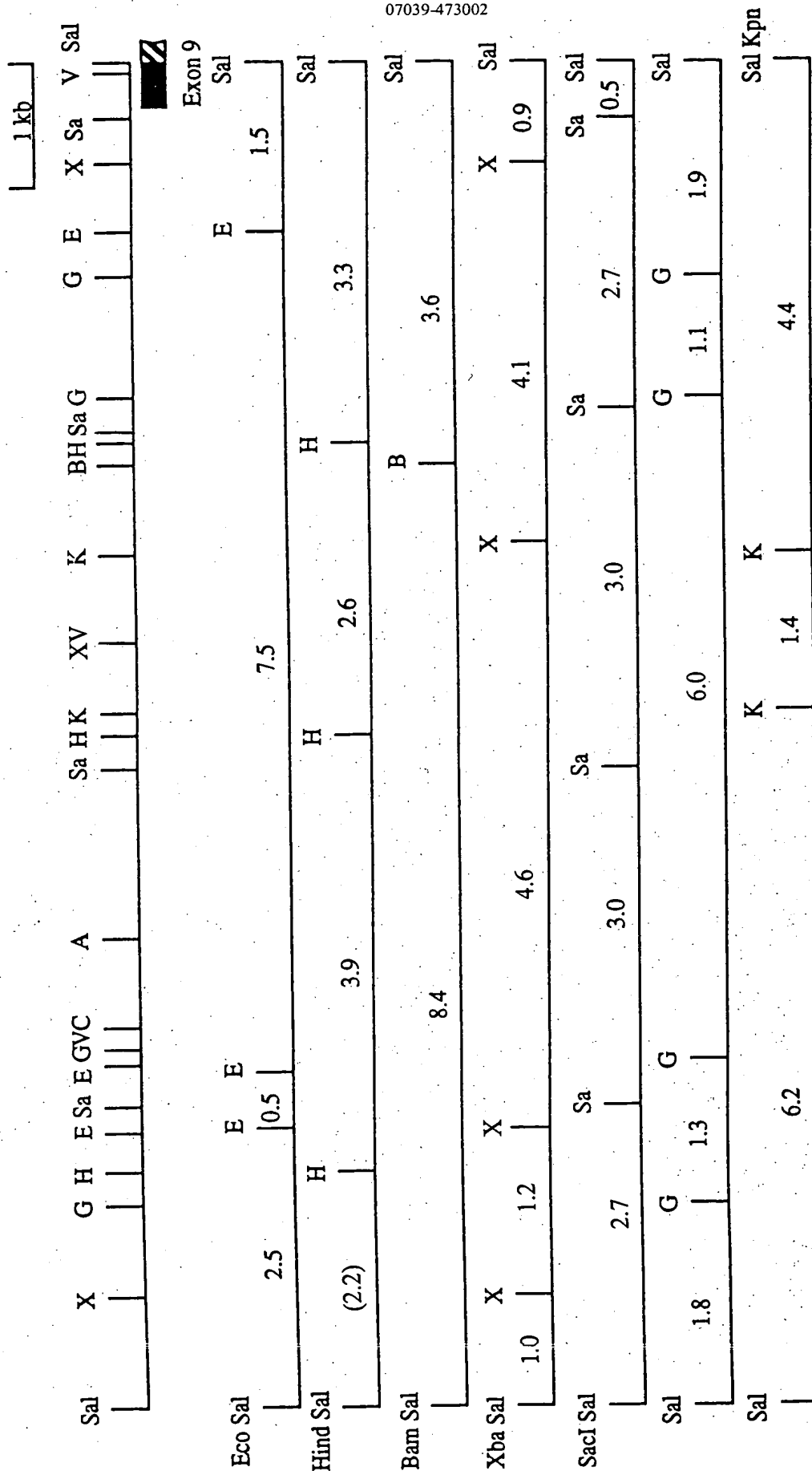


FIG. 10a

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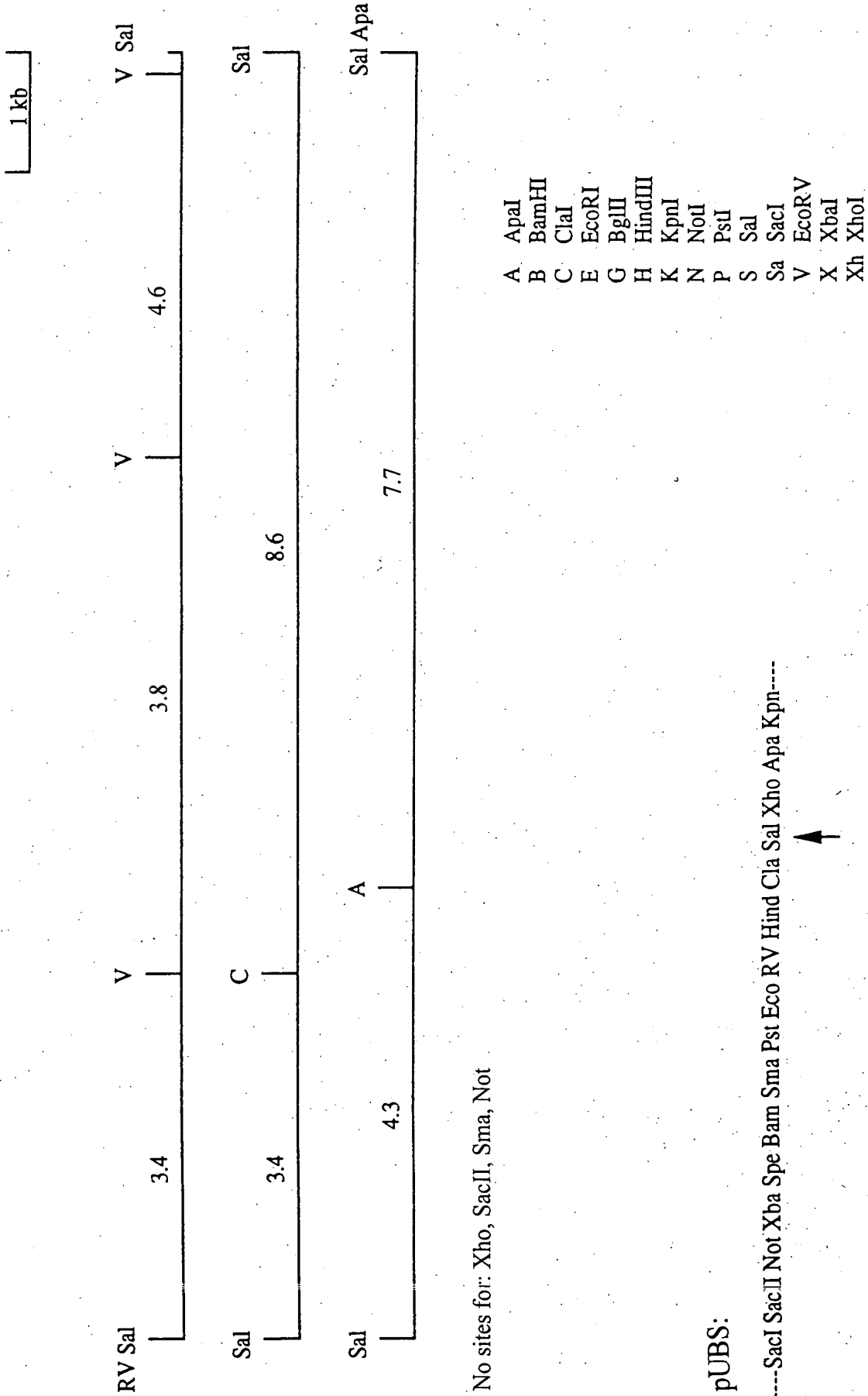


FIG. 10b

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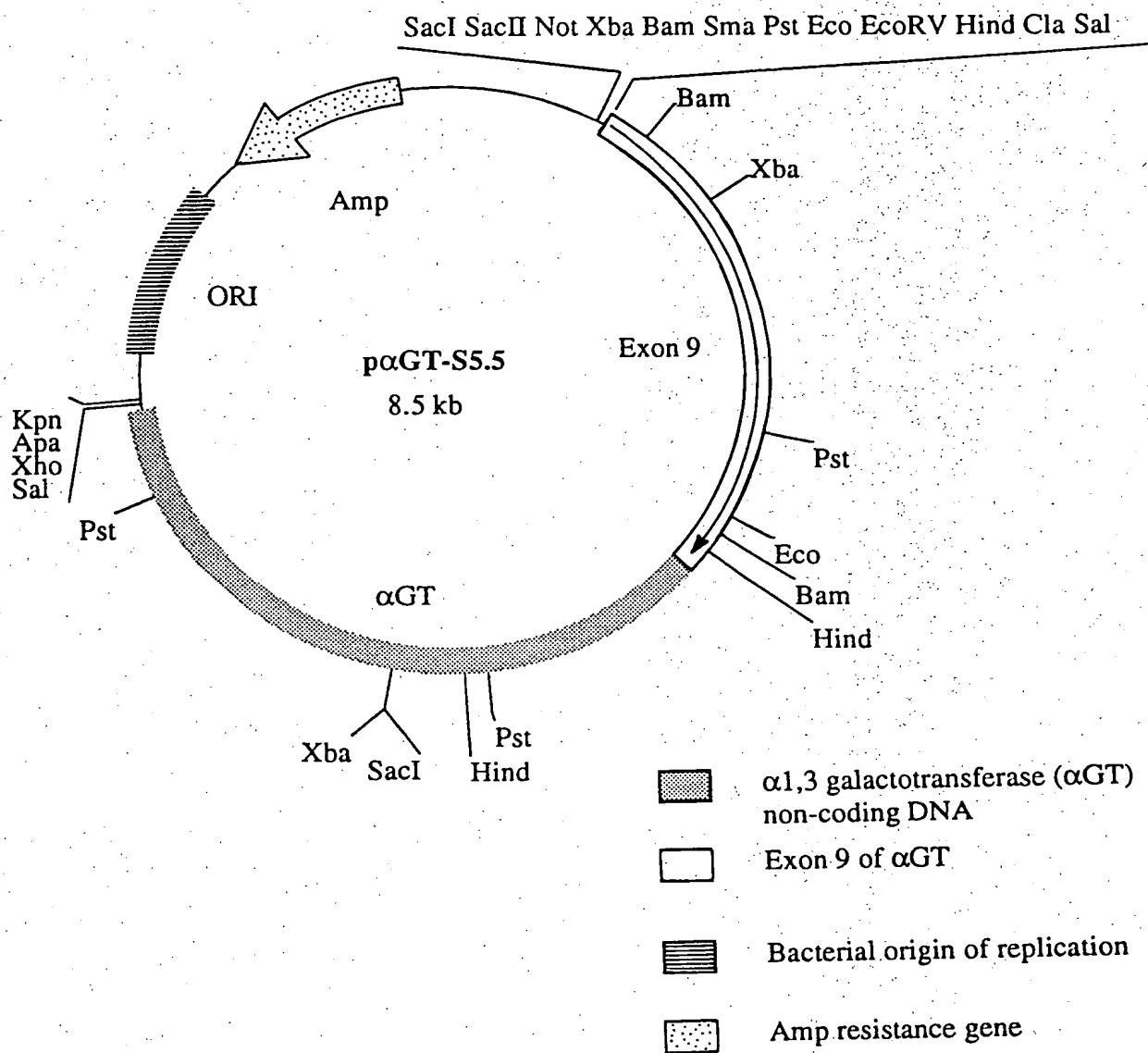


FIG. II

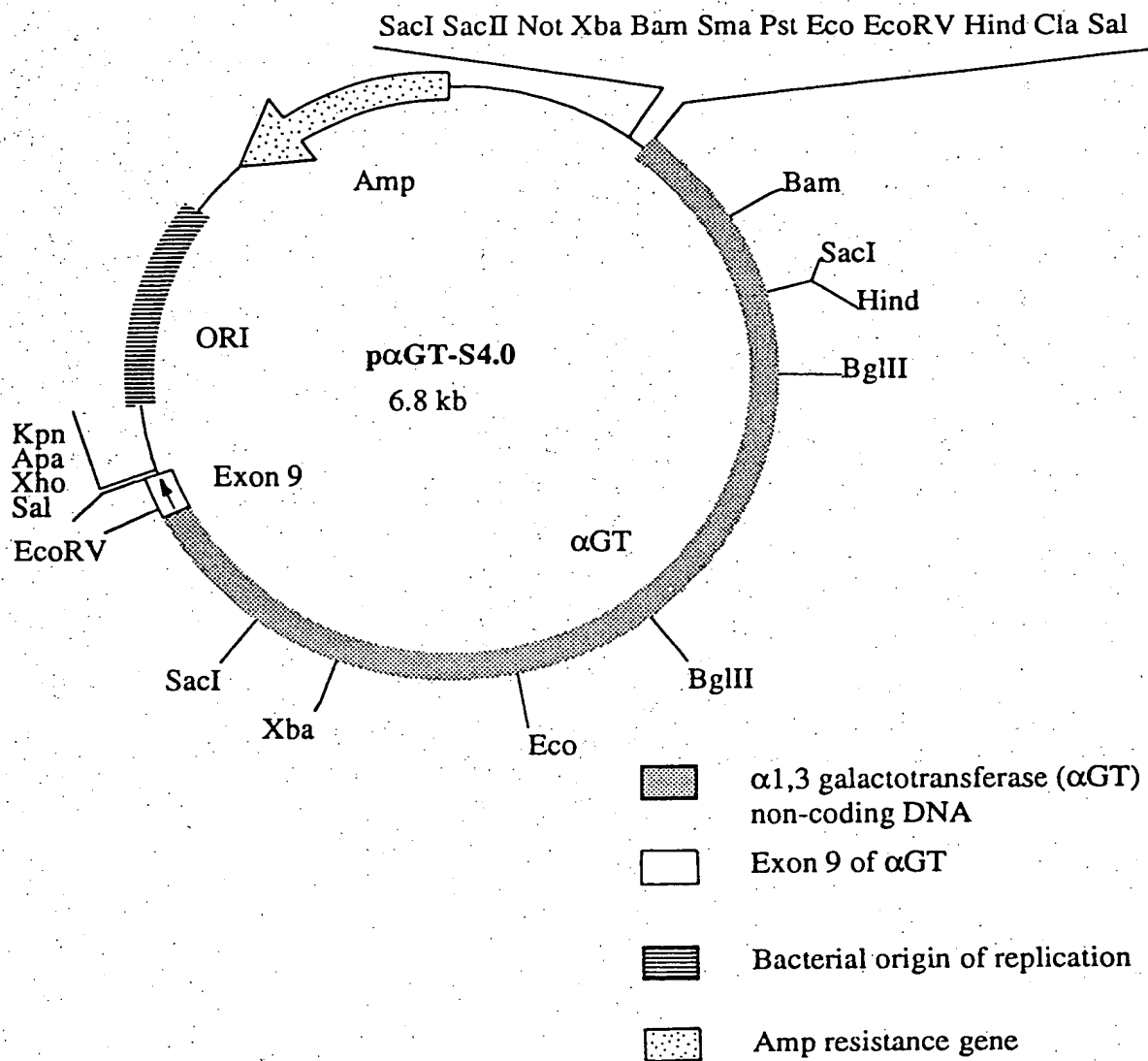


FIG. 12

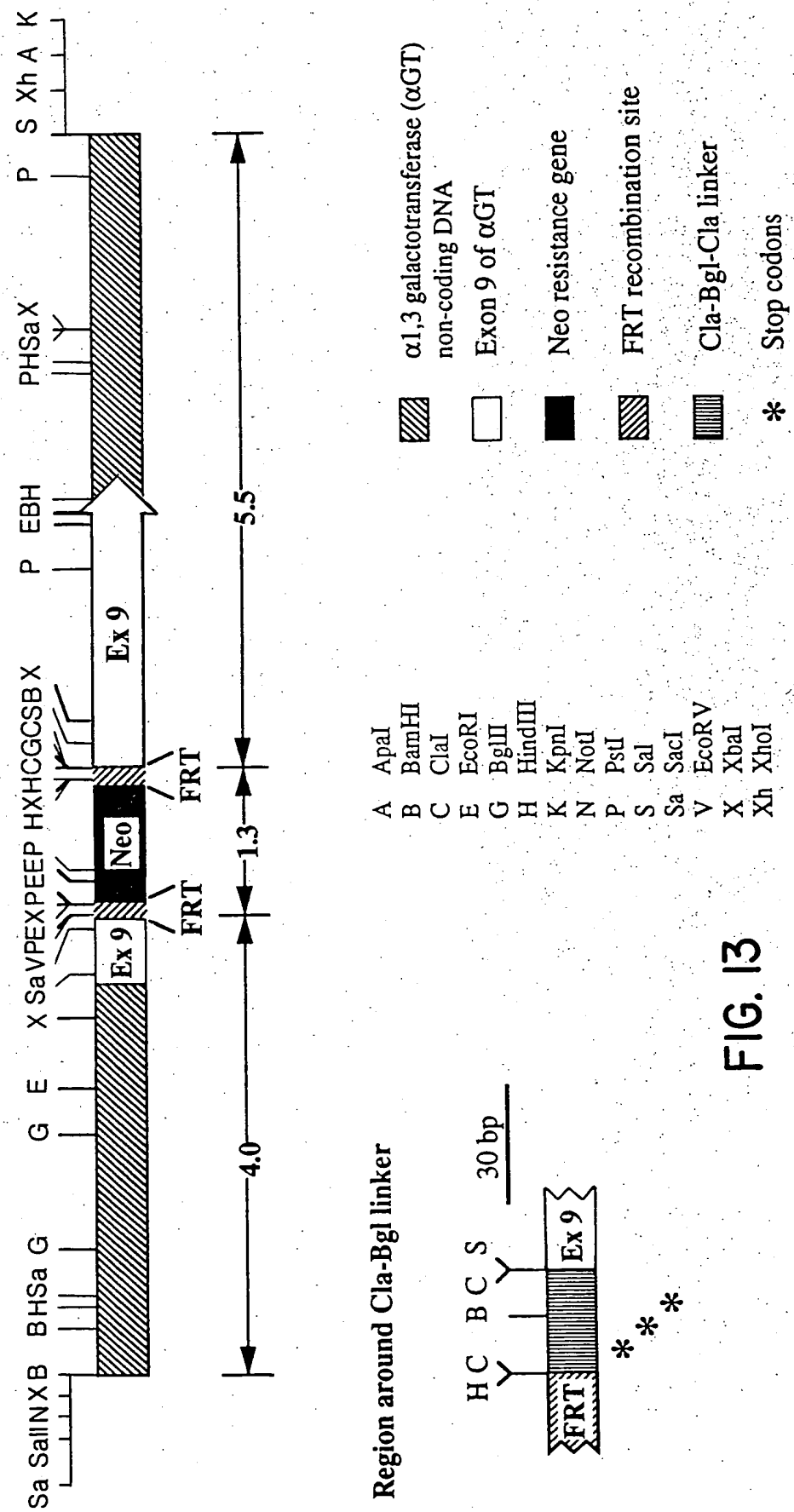


FIG. 13

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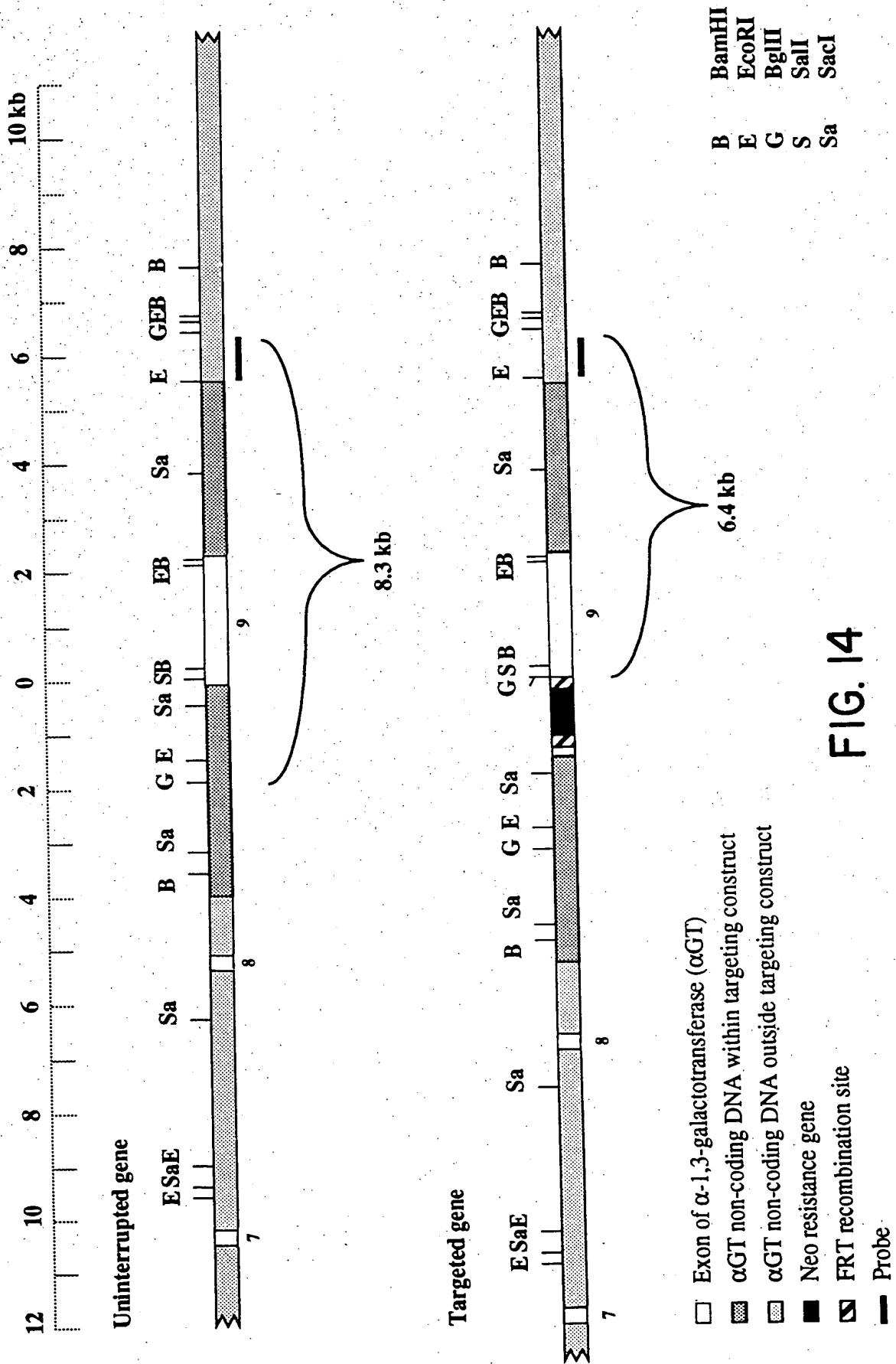


FIG. 14

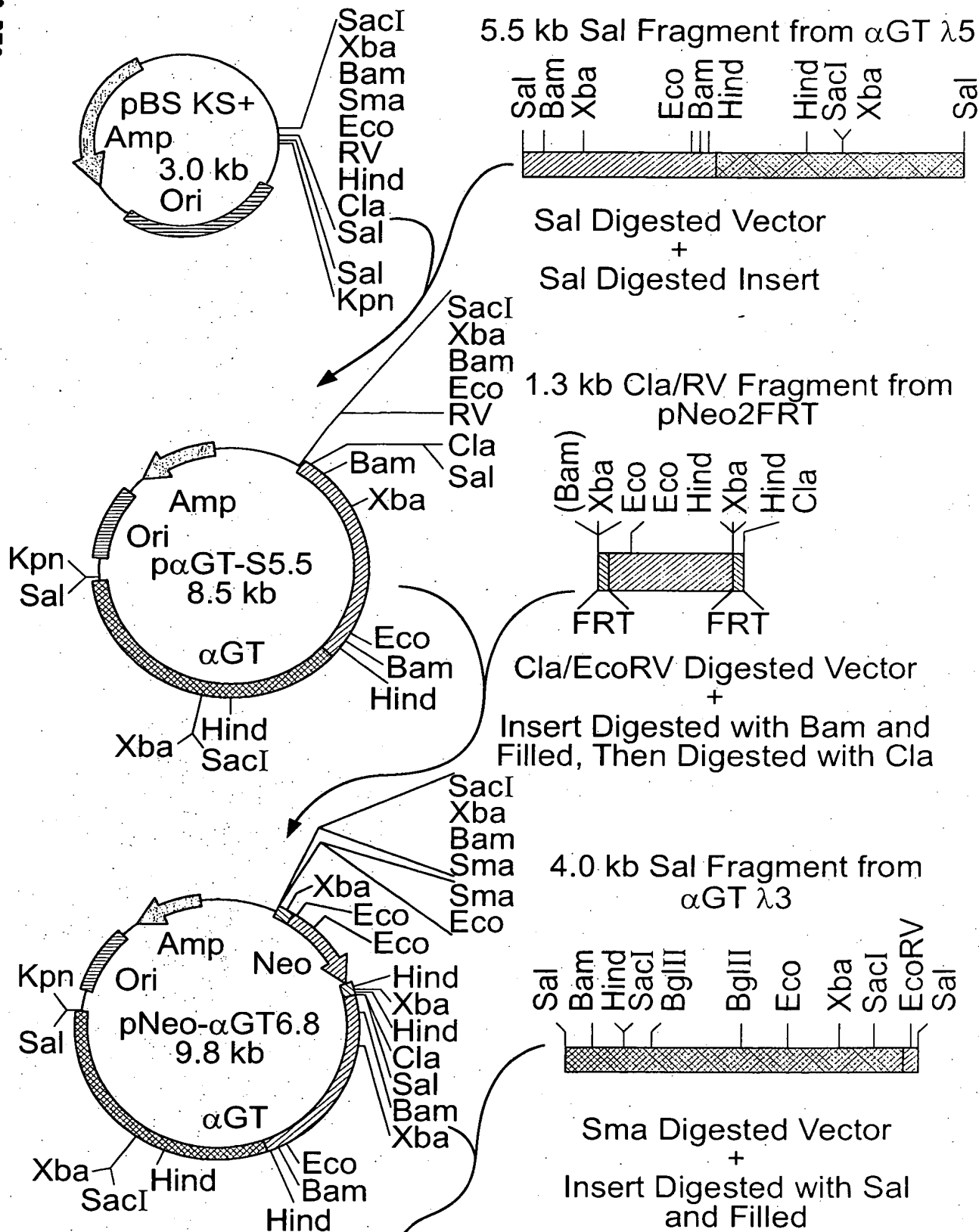


FIG. 15A

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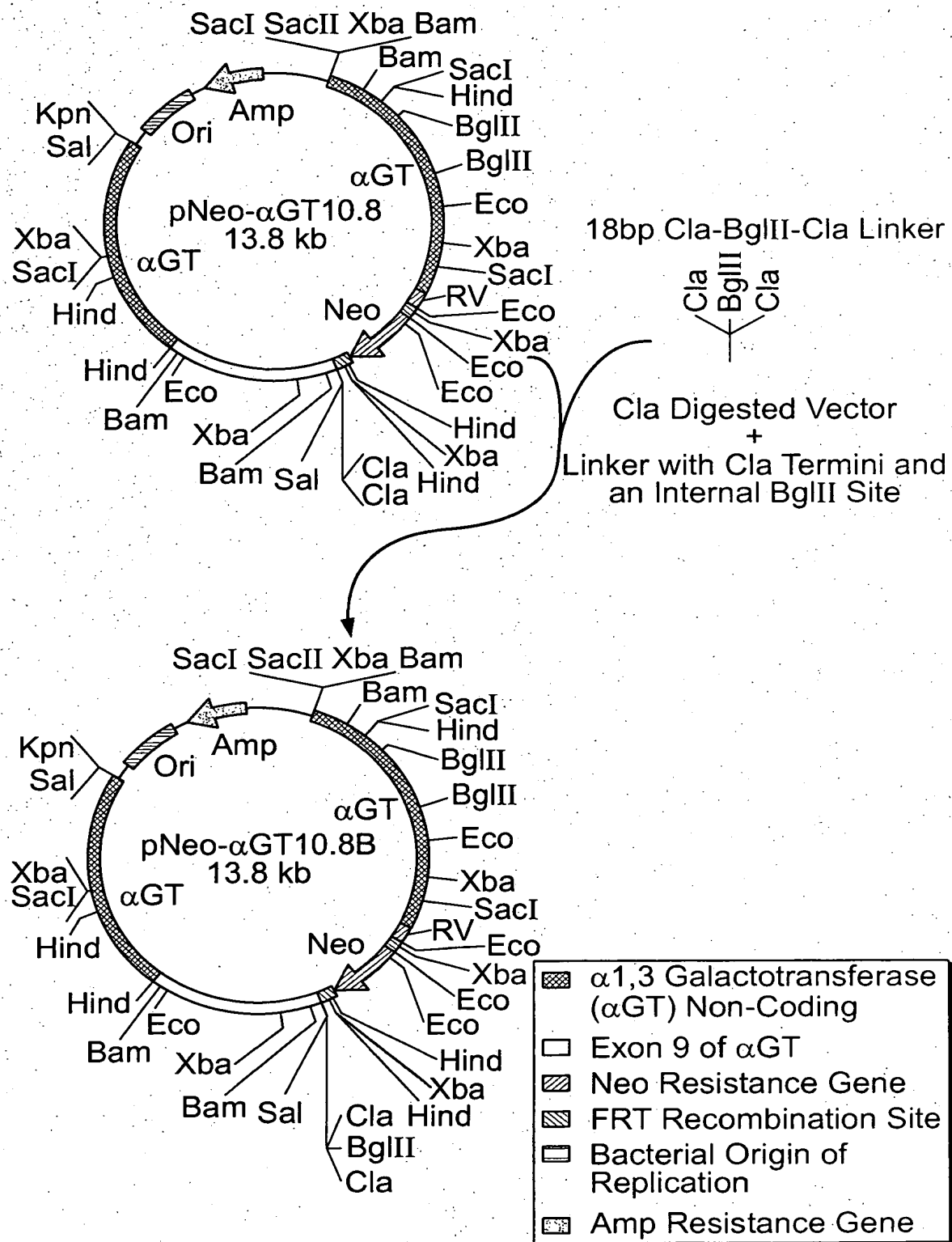


FIG. 15B



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10	20	30	40	50	60
GAGGGCTGCA	GGAATTCGAT	GATCCCCCAG	CTTGAAGTTC	CTATTCCGAA	GTTCTTATTC
70	80	90	100	110	120
TCTAGAAAGT	ATAGGAACTT	CAAGCTGGGC	TGCAGGAATT	CGATTTCGAGC	AGTGTGGTTT
130	140	150	160	170	180
TGCAAGAGGA	AGCAAAAAGC	CTCTCCACCC	AGGCCTGGAA	TGTTTCCACC	CAATGTCGAG
190	200	210	220	230	240
CAGTGTGGTT	TTGCAAGAGG	AAGCAAAAAG	CCTCTCCACC	CAGGCCTGGA	ATGTTTCCAC
250	260	270	280	290	300
CCAATGTGCA	GCAAACCCCG	CCCAGCGTCT	TGTCATTGGC	GAATTCGAAC	ACGCAGATGC
310	320	330	340	350	360
AGTCGGGGCG	GCGCGGTCCC	AGGTCCACTT	GGCATATTAA	GGTGACGCGT	GTGGCCTCGA
370	380	390	400	410	420
ACACCGAGCG	ACCCTGCAGC	CAATATGGGA	TCGGCCATTG	AACAAGATGG	ATTGCACGCA
430	440	450	460	470	480
GGTTCTCCGG	CCGCTTGGGT	GGAGAGGCTA	TTCGGCTATG	ACTGGGCACA	ACAGACAATC
490	500	510	520	530	540
GGCTGCTCTG	ATGCCGCCGT	GTTCCGGCTG	TCAGCGCAGG	GGCGCCCGGT	TCTTTTGTGC
550	560	570	580	590	600
AAGACCGACC	TGTCCGGTGC	CCTGAATGAA	CTCCAAGACG	AGGCAGCGCG	GCTATCGTGG
610	620	630	640	650	660
CTGGCCACGA	CGGGCGTTCC	TTGCGCAGCT	GTGCTCGACG	TTGTCACTGA	AGCGGGAAGG
670	680	690	700	710	720
GACTGGCTGC	TATTGGGCGA	AGTGCCGGGG	CAGGATCTCC	TGTCATCTCA	CCTTGCTCCT
730	740	750	760	770	780
GCCGAGAAAG	TATCCATCAT	GGCTGATGCA	ATGCGGCGGC	TGCATACGCT	TGATCCGGCT
790	800	810	820	830	840
ACCTGCCCAT	TCGACCACCA	AGCGAAACAT	CGCATCGAGC	GAGCACGTAC	TCGGATGGAA
850	860	870	880	890	900
GCCGGTCTTG	TCGATCAGGA	TGATCTGGAC	GAAGAGCATC	AGGGGCTCGC	GCCAGCCGAA
910	920	930	940	950	960
CTGTTGCGCA	GGCTCAAGGC	GCGGATGCCC	GACGGCGAGG	ATCTCGTCGT	GACCCATGGC
970	980	990	1000	1010	1020
GATGCCTGCT	TGCCGAATAT	CATGGTGGA	AATGGCCGCT	TTTCTGGATT	CATCGACTGT
1030	1040	1050	1060	1070	1080
GGCCGGCTGG	GTGTGGCGGA	CCGCTATCAG	GACATAGCGT	TGGCTACCCG	TGATATTGCT
1090	1100	1110	1120	1130	1140
GAAGAGCTTG	GCGGCGAATG	GGCTGACCGC	TTCTCTGTGC	TTTACGGTAT	CGCCGCTCCC

FIG. 16A

1150	1160	1170	1180	1190	1200
GATTCGCAGC	GCATCGCCTT	CTATCGCCTT	CTTGACGAGT	TCTTCTGAGG	GGATCGGCAA
1210	1220	1230	1240	1250	1260
TAAAAAGACA	GAATAAAACG	CACGGGTGTT	GGGCGTTTGT	TCGGATCATC	AAGCTTGAAG
1270	1280	1290	1300	1310	1320
TTCCTATTCC	GAAGTTCCTA	TTCTCTAGAA	AGTATAGGAA	CTTCAAGCTT	ATCGATGAGT
1330	1340	1350	1360	1370	1380
AGATCTTGAT	CGATACCGTC

Linker sequences : 0-28

FRT : 29-104

Polyoma virus enhancer repeats : 105-249

Herpes Simplex Virus Tyrosine Kinase promoter : 250-385

Neomycin phosphotransferase coding region : 385-1188

Herpes Simplex Virus Tyrosine Kinase PolyA signal : 1189-1249

FRT : 1250-1310

Linker sequences : 1311-1340

FIG. 16B

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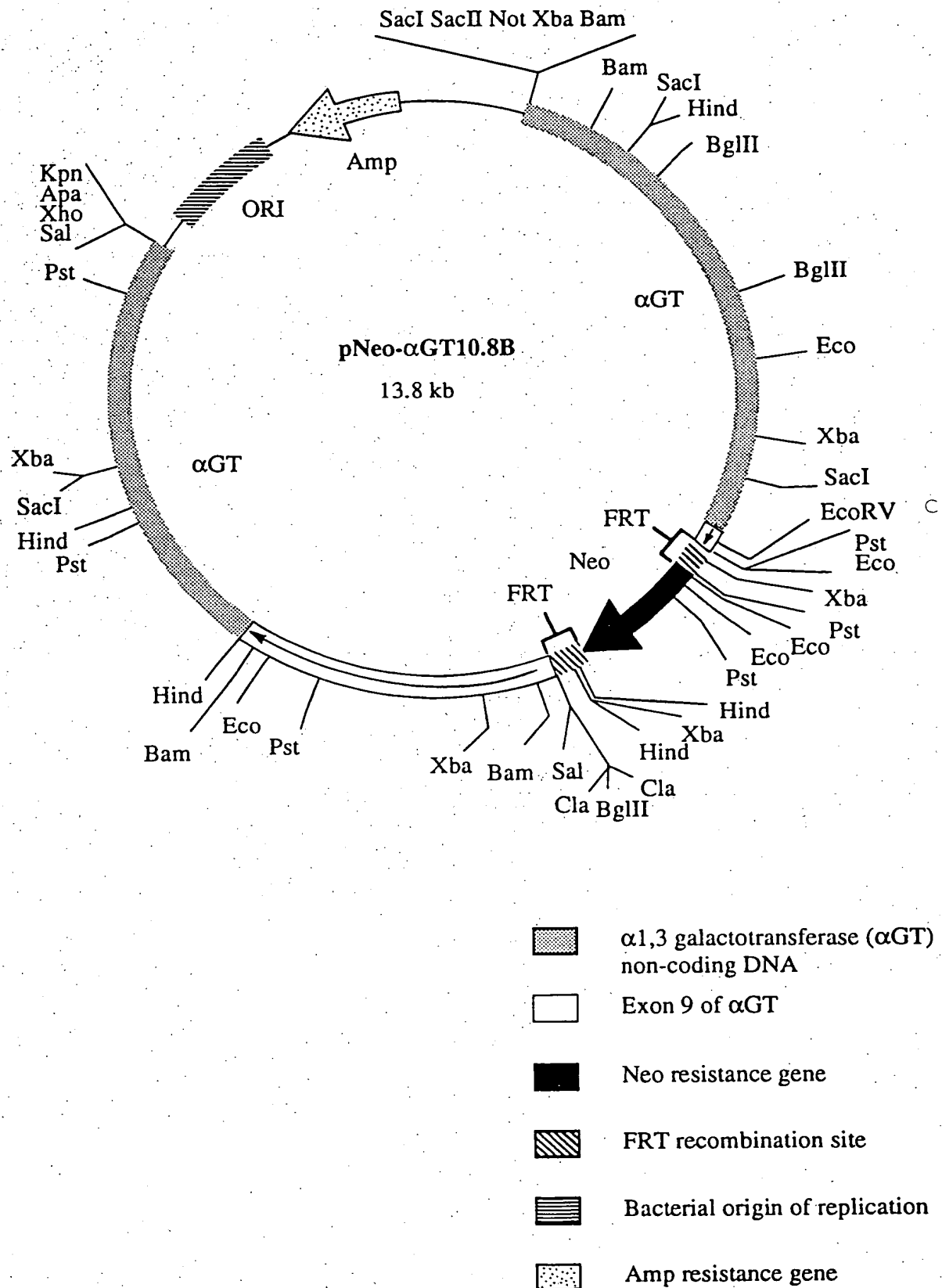


FIG. 17

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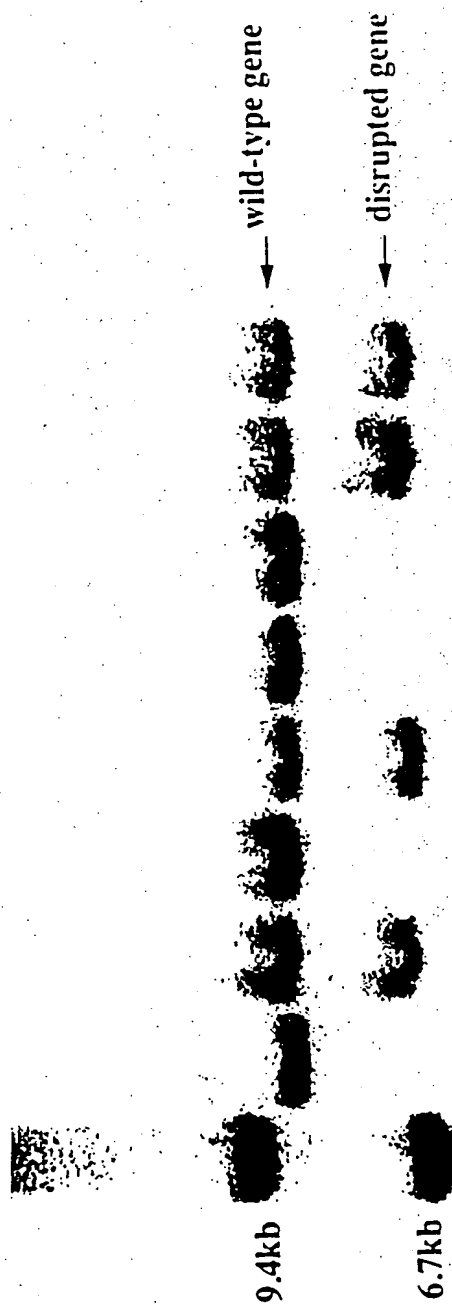


FIG. 18

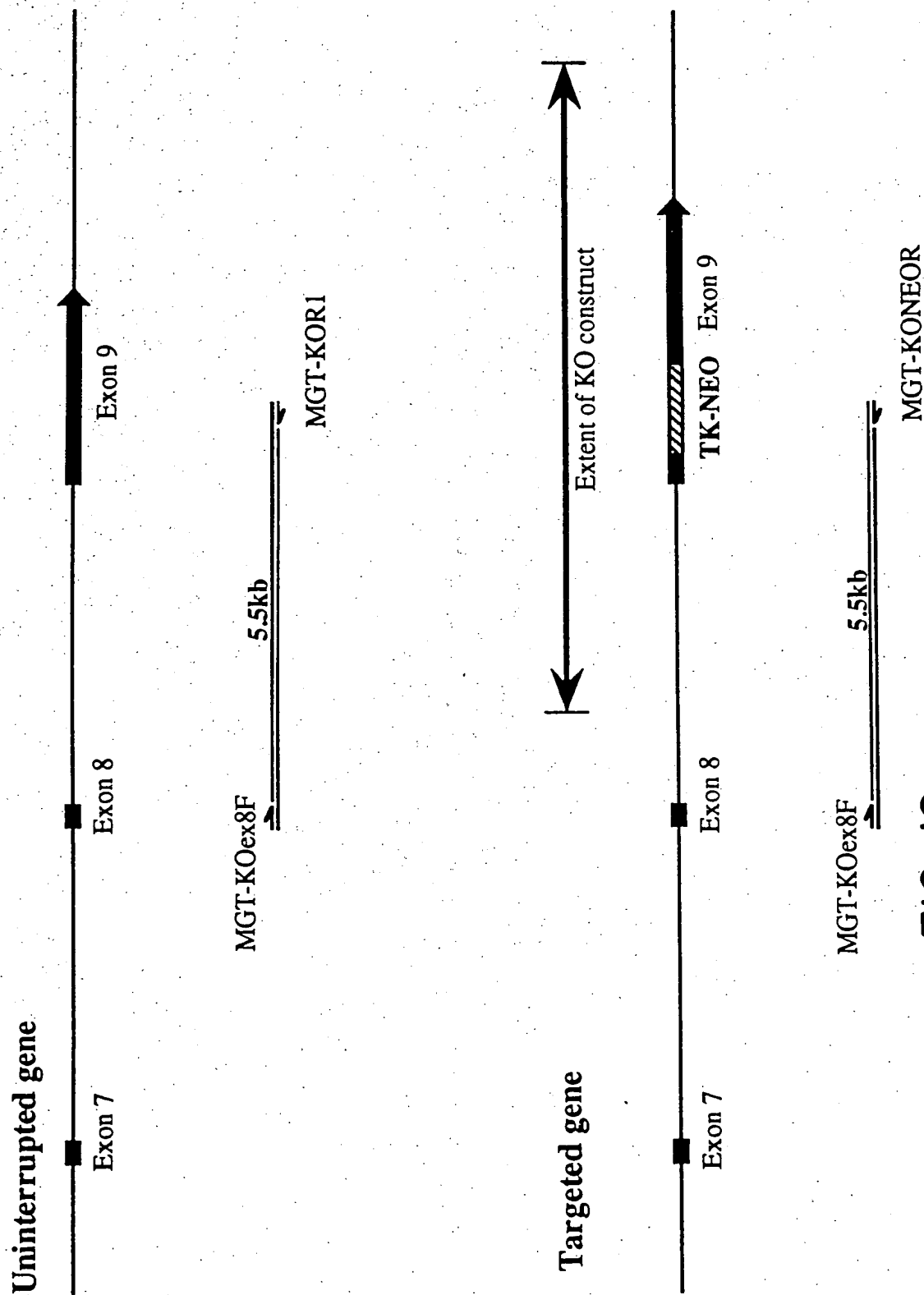
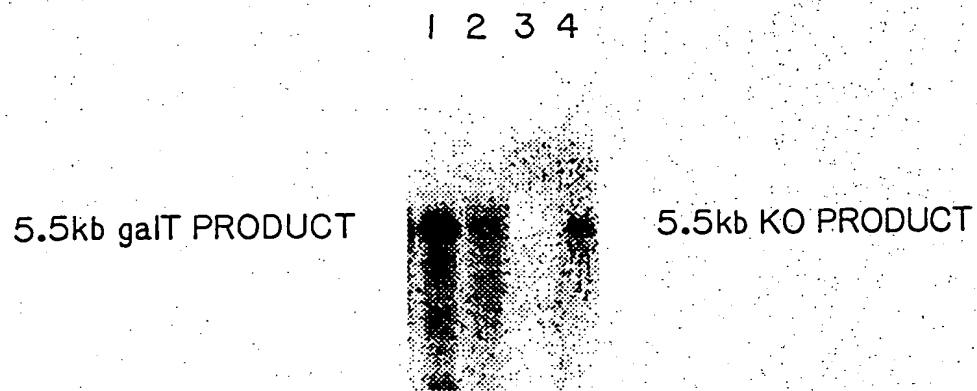


FIG. 19

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1. CBAC TEMPLATE; WILD TYPE PRIMERS
2. 7C2 TEMPLATE; WILD TYPE PRIMERS
3. CBAC TEMPLATE; KO PRIMERS
4. 7C2 TEMPLATE; KO PRIMERS

FIG. 20

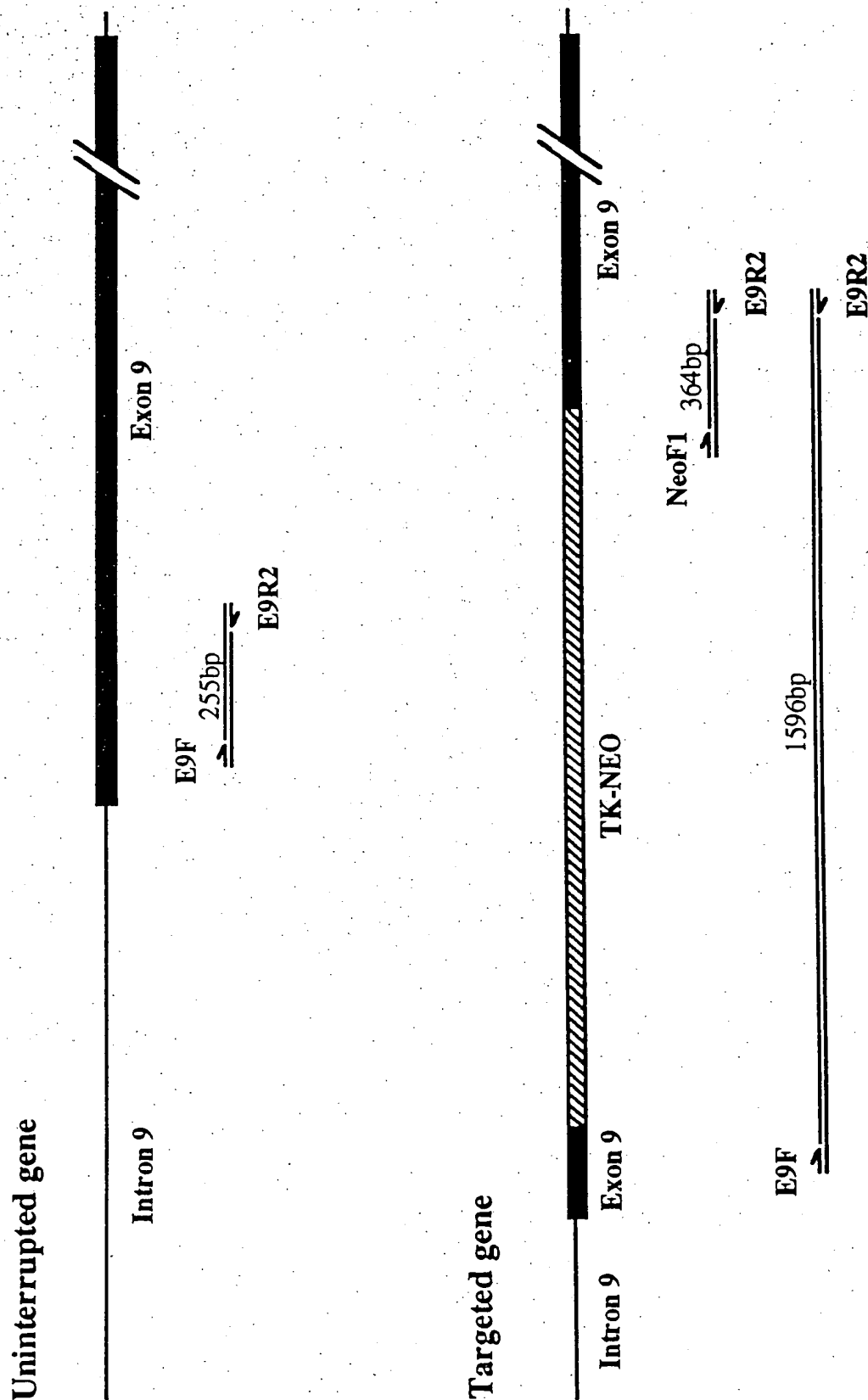


FIG. 2I



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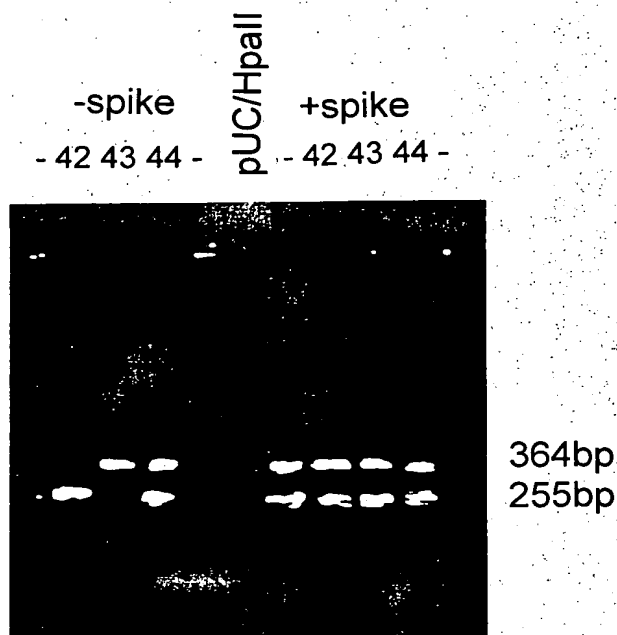


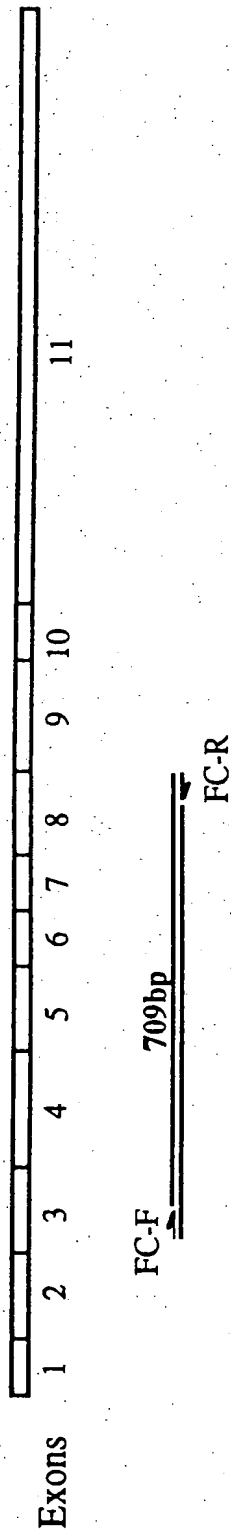
FIG. 22



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Primer binding sites within mouse ferrochelatase cDNA



Primer binding sites within mouse α -1,3-GalT cDNA

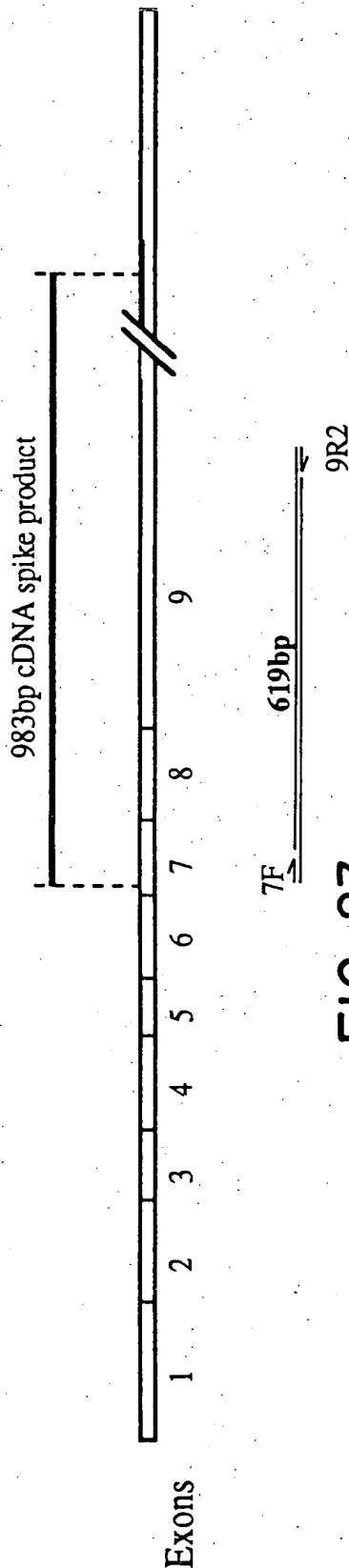


FIG. 23



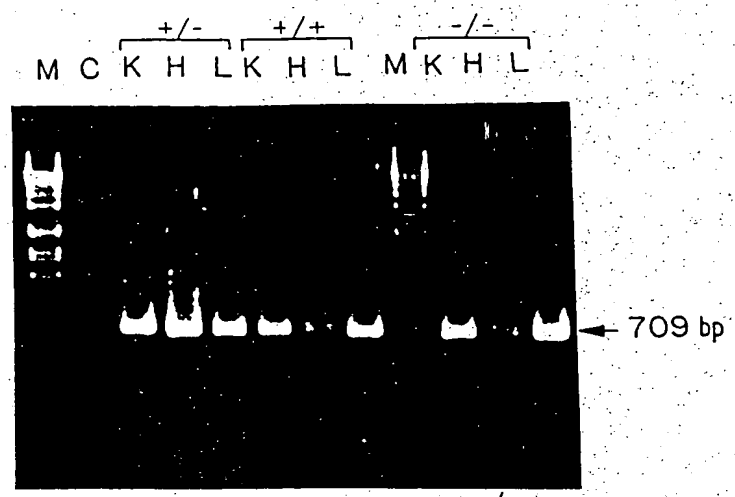
012004

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i) Ferrochelatase, FC-F/R

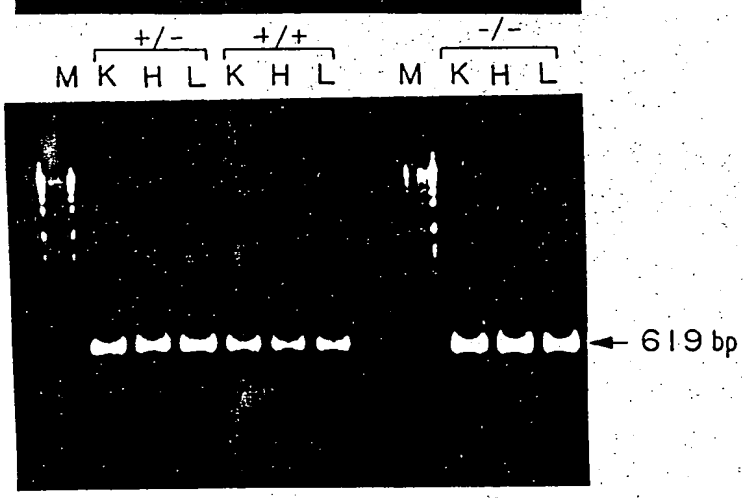
M, Marker SPP-I
C, MQW control
K, KIDNEY
H, HEART
L, LIVER

FIG. 24a



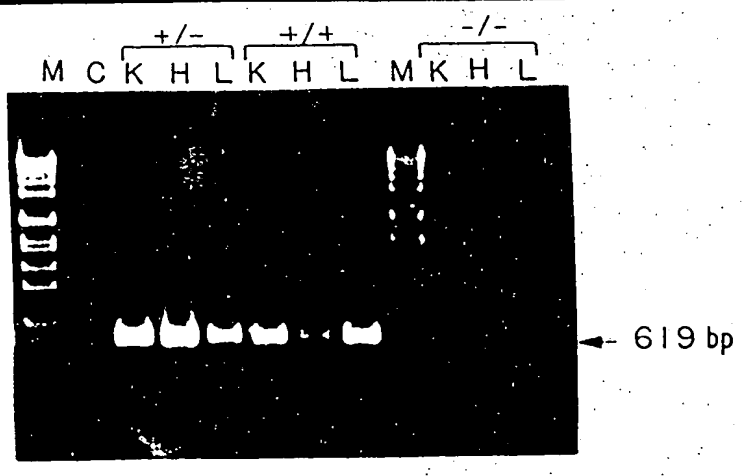
ii) α -1,3-GT cDNA spike
+ 7F/9R2 primers

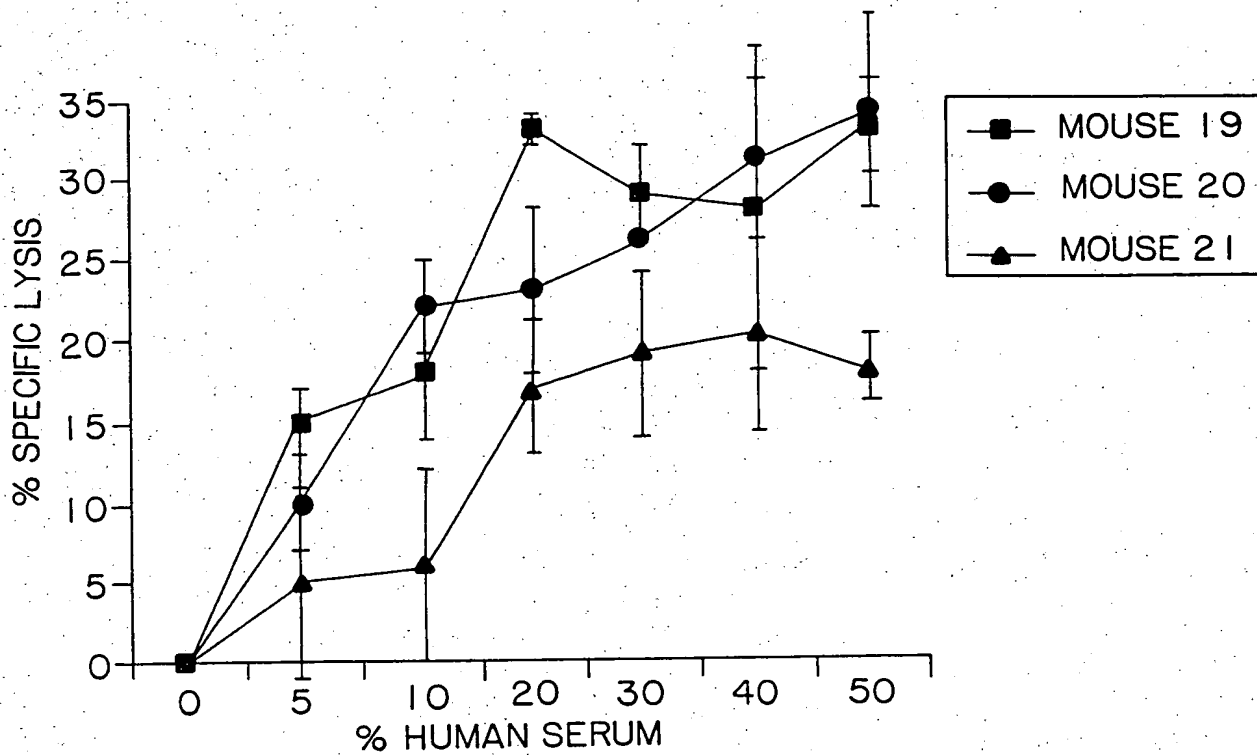
FIG. 24b



iii) α -1,3-GT
7F/9R2 primers

FIG. 24c





MOUSE 19: WILD TYPE; MOUSE 20: HETEROZYGOTIC Gal KO; MOUSE 21:
HOMOZYGOUS Gal KO

FIG. 25

T-LIF SEQUENCE - Murine

CTGACACCTTTGCTTTCTCTTGC GTGTCCGCCTGCGACCTTTCCCCACCCC
GGCCTCTTTCTGGTTGCACCACTTCTCTCATTCCAAAGGATTGTGCCCTTA
CTGCTGCTGGTTCTGCACTGGAAACACGGGGCAGGGAGCCCTCTTCCCATCAC
CCCTGTAAATGCCACCTGTGCCATACGCCACCCATGCCACGGCAACCTC

Met Asn Gln Ile Lys Asn Gln Leu Ala Gln Leu Asn Gly
ATG AAC CAG ATC AAG AAT CAA CTG GCA CAG CTC AAT GGC

Ser Ala Asn Ala Leu Phe Ile Ser Tyr Tyr Thr Ala Gln Gly
AGC GCC AAT GCT CTC TTC ATT TCC TAT TAC ACA GCT CAA GGX

Glu Pro Phe Pro Asn Asn Val Glu Lys Leu Cys Ala Pro Asn
GAG CCG TTT CCC AAC AAC GTG GAA AAG CTA TGT GCG CCT AAC

Met Thr Asp Phe Pro Ser Phe His Gly Asn Gly Thr Glu Lys
ATG ACA GAC TTC CCA TCT TTC CAT GGC AAC GGG ACA GAG AAG

Thr Lys Leu Val Glu Leu Tyr Arg Met Val Ala Tyr Leu Ser
ACC AAG TTG GTG GAG CTG TAT CGG ATG GTC GCA TAC CTG AGC

Ala Ser Leu Thr Asn Ile Thr Arg Asp Gln Lys Val Leu Asn
GCC TCC CTG ACC AAT ATC ACC CGG GAC CAG AAG GTC CTG AAC

Pro Thr Ala Val Ser Leu Gln Val Lys Leu Asn Ala Thr Ile
CCC ACT GCC GTG AGC CTC CAG GTC AAG CTC AAT GCT ACT ATA

Asp Val Met Arg Gly Leu Leu Ser Asn Val Leu Cys Arg Leu
GAC GTC ATG AGG GGC CTC CTC AGC AAT GTG CTT TGC CGT CTG

Cys Asn Lys Tyr Arg Val Gly His Val Asp Val Pro Pro Val
TGC AAC AAG TAC CGT GTG GGC CAC GTG GAT GTG CCA CCT GTC

Pro Asp His Ser Asp Lys Glu Ala Phe Gln Arg Lys Lys Leu
CCC GAC CAC TCT GAC AAA GAA GCC TTC CAA AGG AAA AAG TTG

Gly Cys Gln Leu Leu Gly Thr Tyr Lys Gln Val Ile Ser Val
GGT TGC CAG CTT CTG GGG ACA TAC AAG CAA GTC ATA AGT GTG

Val Val Gln Ala Phe ***
GTG GTC CAG GCC TTC TAG AGAGGAGGTCTTGAATGTACCATGGACTG...

FIG. 26

GACCTTTTGC CTTTCTCTC TCCTGGTGCA CCATTTCTC TCCCTCCCTG 50
AGCCGGAGTT GTGCCCCTGC TGTGGTTCT GCACTGGAAA CATGGGGCGG 100
GGAGCCCCCT CCCCATCACC CCTGTCAACG CCACCTGTGC CACACGCCAC 150
CCATGTCACA ACAACCTC ATG AAC CAG ATC 182
Met Asn Gln Ile
AGG AGC CAA CTG GCA CAG CTC AAT GGC AGT GCC AAT GCC CTC 227
Arg Ser Gln Leu Ala Gln Leu Asn Gly Ser Ala Asn Ala Leu
5 10 15
TTT ATT CTC TAT TAC ACA GCC CAG GGG GAG CCG TTC CCC AAC 272
Phe Ile Leu Tyr Tyr Thr Ala Gln Gly Glu Pro Phe Pro Asn
20 25 30
AAC CTG GAC AAG CTA TGT GGC CCC AAC GTG ACG GAC TTC CCG 317
Asn Leu Asp Lys Leu Cys Gly Pro Asn Val Thr Asp Phe Pro
35 40 45
CCC TTC CAC GCC AAC GGC ACG GAG AAG GCC AAG CTG GTG GAG 362
Pro Phe His Ala Asn Gly Thr Glu Lys Ala Lys Leu Val Glu
50 55 60
CTG TAC CGC ATA GTC GTG TAC CTT GGC ACC TCC CTG GGC AAC 407
Leu Tyr Arg Ile Val Val Tyr Leu Gly Thr Ser Leu Gly Asn
65 70
ATC ACC CGG GAC CAG AAG ATC CTC AAC CCC AGT GCC CTC AGC 452
Ile Thr Arg Asp Gln Lys Ile Leu Asn Pro Ser Ala Leu Ser
75 80 85
CTC CAC AGC AAG CTC AAC GCC ACC GCC GAC ATC CTG CGA GGC 497
Leu His Ser Lys Leu Asn Ala Thr Ala Asp Ile Leu Arg Gly
90 95 100
CTC CTT AGC AAC GTG CTG TGC CGC CTG TGC AGC AAG TAC CAC 542
Leu Leu Ser Asn Val Leu Cys Arg Leu Cys Ser Lys Tyr His
105 110 115
GTG GGC CAT GTG GAC GTG ACC TAC GGC CCT GAC ACC TCG GGT 587
Val Gly His Val Asp Val Thr Tyr Gly Pro Asp Thr Ser Gly
120 125 130
AAG GAT GTC TTC CAG AAG AAG AAG CTG GGC TGT CAA CTC CTG 632
Lys Asp Val Phe Gln Lys Lys Lys Leu Gly Cys Gln Leu Leu
135 140
GGG AAG TAT AAG CAG ATC ATC GCC GTG TTG GCC CAG GCC TTC 677
Gly Lys Tyr Lys Gln Ile Ile Ala Val Leu Ala Gln Ala Phe
145 150 155
TAG CAGGAGGTCT 722

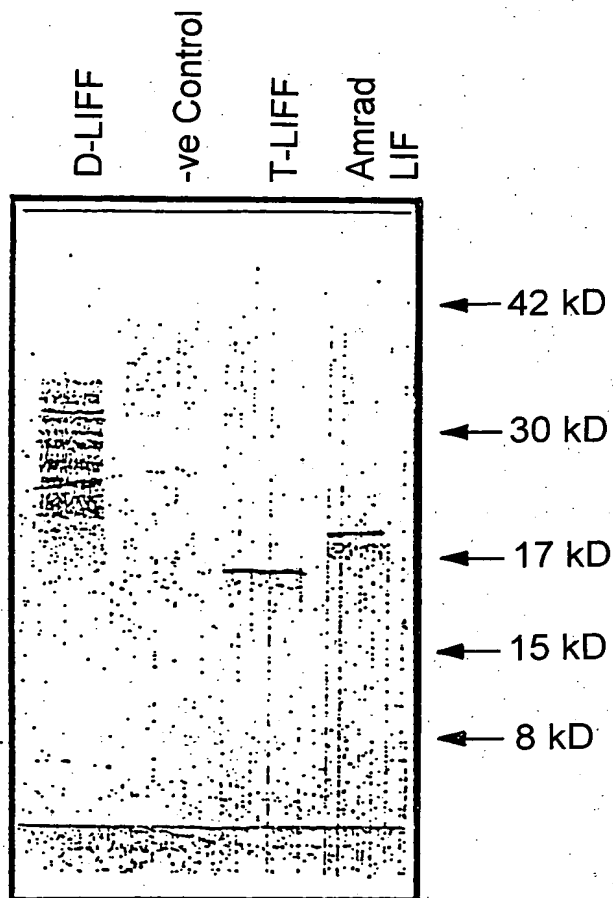
FIG. 27



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FIG. 28



489 bp —
404 bp —
331 bp —
242 bp —
190 bp —
147 bp —
111 bp —

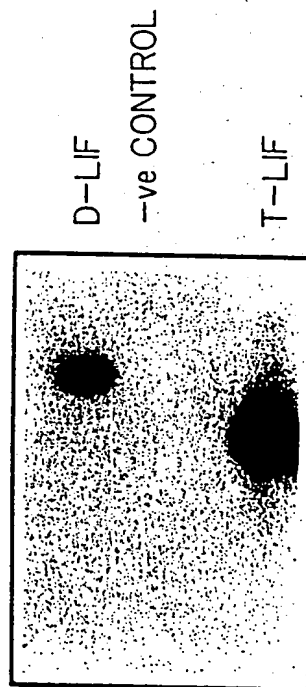
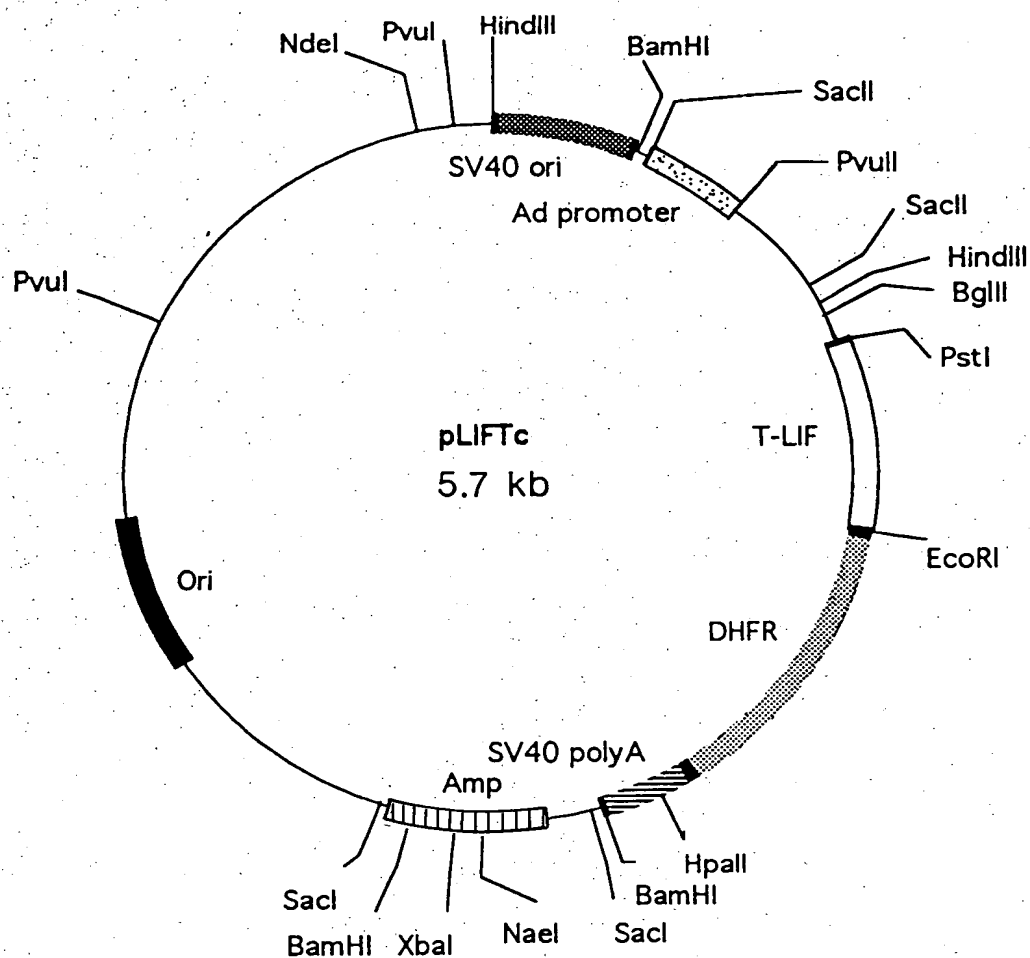


FIG. 30

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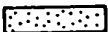



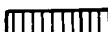
-  Dihydrofolate reductase 3' end
-  Adenovirus promoter
-  SV40 origin of replication
-  T-LIF coding region
-  Bacterial origin of replication
-  Ampicillin resistance gene

FIG. 29